

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 18:52:35 ; Search time 1352 seconds  
(without alignments) 2455.677 Million cell updates/sec

Title: US-09-375-514-22  
Perfect score: 1104  
Sequence: 1 MAHAGRTGYDNRIVMKYIH.....HTWIQDNGWGWGASGDVSLG 205

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60362

Minimum DB seq length: 10  
Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool/US09375514/runat\_28052003.165345.18673/app\_query.fasta\_1.391  
-DB=EST -QPMF=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=10 -MAXLEN=40  
-USER=US09375514.@CNG.1.1.1525.@runat\_28052003.165345.18673 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST :  
1: em\_estba :  
2: em\_esthum :  
3: em\_estin :  
4: em\_estma :  
5: em\_estov :  
6: em\_estpl :  
7: em\_estro :  
8: em\_hic :  
9: gb\_estl :  
10: gb\_est2 :  
11: gb\_hic :  
12: gb\_est3 :  
13: gb\_est4 :  
14: gb\_est5 :  
15: em\_estfun :  
16: em\_estom :  
17: gb\_gss :  
18: em\_gss\_hum :  
19: em\_gss\_inv :  
20: em\_gss\_pln :  
21: em\_gss\_vrt :  
22: em\_gss\_fun :  
23: em\_gss\_man :  
24: em\_gss\_mus :  
25: em\_gss\_other :  
26: em\_gss\_pro :  
27: em\_gss\_rod :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	44	4.0	31	9	AA999756	AA999756 os93e04.s
C 2	42	3.8	34	9	AI811024	AI811024 tr03a03.x
C 3	42	3.8	37	9	AI698327	AI698327 tx63c12.x
C 4	41	3.7	34	9	AI202980	AI202980 qr32e08.x
C 5	41	3.7	40	9	AI628006	AI628006 ty21a06.x
C 6	40	3.6	31	9	AI422710	AI422710 tf29d12.x
C 7	40	3.6	36	13	BM010450	BM010450 603631395
C 8	40	3.6	36	13	BM010792	BM010792 603629306
C 9	40	3.6	37	9	AI683252	AI683252 tx02e12.x
C 10	40	3.6	40	2	HSM003700	AI039224 Homo sapi
C 11	39	3.5	27	17	AZ782295	AZ782295 2M0022019
C 12	39	3.5	34	12	BE729288	BE729288 601561653
C 13	38	3.4	31	9	AI912532	AI912532 tz25g07.x
C 14	38	3.4	34	9	AI131930	AI131930 uc33g07.r
C 15	38	3.4	35	17	AZ832681	AZ832681 2M0113H24
C 16	38	3.4	36	10	BE395744	BE395744 601311259
C 17	38	3.4	37	17	AZ580135	AZ580135 1M0368E16
C 18	38	3.4	40	12	BG709439	BG709439 602673496
C 19	37	3.4	29	17	AZ780387	AZ780387 2M0017N12
C 20	37	3.4	33	17	AZ784258	AZ784258 2M0026G22
C 21	37	3.4	34	9	AI217993	AI217993 qf52g10.x
C 22	37	3.4	34	9	AI362411	AI362411 qv92e02.x
C 23	37	3.4	34	9	AI612902	AI612902 ty33d03.x
C 24	37	3.4	37	9	AI761879	AI761879 wg68c11.x
C 25	37	3.4	40	9	AI015468	AI015468 cv54e11.s
C 26	37	3.4	40	9	AI800161	AI800161 tr23b08.x
C 27	36	3.3	24	17	AZ982483	AZ982483 2M0263K16
C 28	36	3.3	27	10	AW250272	AW250272 2821187.5
C 29	36	3.3	31	9	AA871994	AA871994 o105c06.s
C 30	36	3.3	31	9	AA999756	AA999756 os93e04.s
C 31	36	3.3	31	9	AI677781	AI677781 wc80c06.x
C 32	36	3.3	32	13	BI762555	BI762555 603048685
C 33	36	3.3	32	13	BI832949	BI832949 603090781
C 34	36	3.3	32	13	BI833158	BI833158 603090881
C 35	36	3.3	32	13	BI833514	BI833514 603088181
C 36	36	3.3	32	17	AZ320746	AZ320746 1M0040P21
C 37	36	3.3	33	13	BI829654	BI829654 603079396
C 38	36	3.3	34	9	AI589397	AI589397 tr61h11.x
C 39	36	3.3	35	12	BE867678	BE867678 601443224
C 40	36	3.3	35	17	AZ477888	AZ477888 1M0297B02
C 41	36	3.3	36	17	BH792266	BH792266 SALK_0632
C 42	36	3.3	37	9	AA987401	AA987401 oq87g06.s
C 43	36	3.3	37	9	AI357425	AI357425 qu01c09.x
C 44	36	3.3	38	13	BI829358	BI829358 603079491
C 45	36	3.3	40	9	AA869375	AA869375 vq07c10.r
C 46	36	3.3	40	9	AI565182	AI565182 tq56h10.x
C 47	36	3.3	40	17	AZ372178	AZ372178 1M0123J24
C 48	35.5	3.2	38	12	BE867536	BE867536 601443035
C 49	35	3.2	25	9	AI024239	AI024239 ov71g02.s
C 50	35	3.2	30	17	AZ791470	AZ791470 2M0041H21
C 51	35	3.2	30	17	TA211A03P	TA211A03P qu09a10.x
C 52	35	3.2	31	9	AI273865	AI273865 qu09a10.x
C 53	35	3.2	31	9	AI287914	AI287914 qul13c06.x
C 54	35	3.2	31	9	AI364457	AI364457 qw38e11.x
C 55	35	3.2	34	9	AA625403	AA625403 af69a08.r
C 56	35	3.2	37	13	BI765481	BI765481 603050546
C 57	35	3.2	38	17	AZ313639	AZ313639 1M0030K04
C 58	35	3.2	39	13	BG973894	BG973894 602843523
C 59	35	3.2	39	14	T17564	T17564 mps v232 Th
C 60	35	3.2	40	9	AA034448	AA034448 zk23a08.s
C 61	35	3.2	40	9	AA878864	AA878864 of84g05.s
C 62	35	3.2	40	9	AI282721	AI282721 qt65c10.x
C 63	34.5	3.1	34	9	AI689593	AI689593 tx84g11.x
C 64	34.5	3.1	34	9	AI915735	AI915735 wg73b11.x

65 34 3.1 25 9 AA878798 of82h02.s  
66 34 3.1 28 9 AI096133 SMOVL3CAN  
67 34 3.1 28 17 AZ303959 1M0003P16  
68 34 3.1 30 17 AZ450779 1M0249K09  
69 34 3.1 31 9 AA871994 o105c06.s  
70 34 3.1 31 9 AI422710 tf29d12.x  
71 34 3.1 33 17 AZ380833 1M0136021  
72 34 3.1 33 17 AZ961620 2M0230809  
73 34 3.1 34 9 AI368216 qv99c06.x  
74 34 3.1 34 9 AA293547 t554g12.s  
75 34 3.1 34 17 AZ591530 1M0401L09  
76 34 3.1 34 17 AZ832181 2M0112K19  
77 34 3.1 34 17 AL759480 Arabidops  
78 34 3.1 35 17 AZ439115 1M0229N05  
79 34 3.1 35 17 AZ469734 1M0283J19  
80 34 3.1 35 17 AZ946037 2M0207G10  
81 34 3.1 36 9 AL655844  
82 34 3.1 37 9 AA931619 oo35a11.s  
83 34 3.1 37 9 AL801867  
84 34 3.1 37 9 AU257109 AU257109  
85 34 3.1 38 17 AZ487251 1M0316A18  
86 34 3.1 38 17 AZ775686 2M0008H12  
87 34 3.1 39 17 AZ445435 1M0241B14  
88 34 3.1 39 17 AZ997025 2M0283J19  
89 34 3.1 40 9 AI088727 qal6e11.x  
90 34 3.1 40 14 D21036  
91 34 3.1 40 17 AZ320260 1M0040A15  
92 33.5 3.0 37 12 BF036425 601460458  
93 33.5 3.0 37 9 AZ275360 vc07404.r  
94 33 3.0 37 9 AZ314511 1M0031B20  
95 33 3.0 19 17 AZ324865 1M0047G10  
96 33 3.0 23 17 AZ861432 2M0167E24  
97 33 3.0 25 17 AZ861588 2M0168J04  
98 33 3.0 26 17 AZ588958 1M0397B09  
99 33 3.0 28 9 AI623372 ts18e04.x  
100 33 3.0 28 9 AI687937  
101 33 3.0 30 17 AZ375563 1M0128P24  
102 33 3.0 30 17 AZ864869 2M0174M09  
103 33 3.0 30 17 AZ995340 2M0281E11  
104 33 3.0 31 9 AI689315 tx93f07.x  
105 33 3.0 31 17 AZ485617 1M0313G08  
106 33 3.0 31 17 DE2122S  
107 33 3.0 33 13 BM398978  
108 33 3.0 33 17 AZ627977 1M0476L03  
109 33 3.0 34 9 AI128655  
110 33 3.0 34 9 AI217993 qf52g10.s  
111 33 3.0 34 9 AI278110 qm63b12.x  
112 33 3.0 34 9 AI396645 fb15d12.x  
113 33 3.0 34 9 AI539355 te51a08.x  
114 33 3.0 34 17 AZ635438 1M0491J15  
115 33 3.0 34 17 BH811595 SALK\_0591  
116 33 3.0 35 13 BJ032206 BJ032206  
117 33 3.0 35 13 BJ080323 BJ080323  
118 33 3.0 35 17 AZ377416 1M0131F13  
119 33 3.0 35 17 AZ454138 1M0256A01  
120 33 3.0 35 17 AZ605156 1M0426A23  
121 33 3.0 36 13 B1111123 602898986  
122 33 3.0 36 17 AZ839832 2M0136D12  
123 33 3.0 36 17 BH813734 SALK\_0652  
124 33 3.0 36 17 BH814198 SALK\_0658  
125 33 3.0 37 9 AI198787 qf79c02.x  
126 33 3.0 37 9 AI572876 tm63c03.x  
127 33 3.0 37 9 AI625989 ar91l09.x  
128 33 3.0 37 9 AI800153 tr23a06.x  
129 33 3.0 37 13 BJ053200 BJ053200  
130 33 3.0 37 17 AZ824496 2M0099C12  
131 33 3.0 38 12 BE867536 601443035  
132 33 3.0 38 17 AZ500372 1M0338M11  
133 33 3.0 39 17 AZ462636 1M0269K12  
134 33 3.0 39 17 BH171128 SALK\_0038  
135 33 3.0 40 9 AA888208 of86c10.s  
136 33 3.0 40 9 AA894396 of85g05.s  
137 33 3.0 40 9 AA961445 or53e03.s

AA878798 of82h02.s  
AI096133 SMOVL3CAN  
AZ303959 1M0003P16  
AZ450779 1M0249K09  
AA871994 o105c06.s  
AI422710 tf29d12.x  
AZ380833 1M0136021  
AZ961620 2M0230809  
AI368216 qv99c06.x  
AA293547 t554g12.s  
AZ591530 1M0401L09  
AZ832181 2M0112K19  
AL759480 Arabidops  
AZ439115 1M0229N05  
AZ469734 1M0283J19  
AZ946037 2M0207G10  
AL655844  
AA931619 oo35a11.s  
AL801867  
AU257109 AU257109  
AZ487251 1M0316A18  
AZ775686 2M0008H12  
AZ445435 1M0241B14  
AZ997025 2M0283J19  
AI088727 qal6e11.x  
D21036  
AZ320260 1M0040A15  
BF036425 601460458  
AZ275360 vc07404.r  
AZ314511 1M0031B20  
AZ324865 1M0047G10  
AZ861432 2M0167E24  
AZ861588 2M0168J04  
AZ588958 1M0397B09  
AI623372 ts18e04.x  
AI687937  
AZ375563 1M0128P24  
AZ864869 2M0174M09  
AZ995340 2M0281E11  
AI689315 tx93f07.x  
AZ485617 1M0313G08  
DE2122S  
BM398978  
AZ627977 1M0476L03  
AI128655  
AI217993 qf52g10.s  
AI278110 qm63b12.x  
AI396645 fb15d12.x  
AI539355 te51a08.x  
AZ635438 1M0491J15  
BH811595 SALK\_0591  
BJ032206 BJ032206  
BJ080323 BJ080323  
AZ377416 1M0131F13  
AZ454138 1M0256A01  
AZ605156 1M0426A23  
B1111123 602898986  
AZ839832 2M0136D12  
BH813734 SALK\_0652  
BH814198 SALK\_0658  
AI198787 qf79c02.x  
AI572876 tm63c03.x  
AI625989 ar91l09.x  
AI800153 tr23a06.x  
BJ053200 BJ053200  
AZ824496 2M0099C12  
BE867536 601443035  
AZ500372 1M0338M11  
AZ462636 1M0269K12  
BH171128 SALK\_0038  
AA888208 of86c10.s  
AA894396 of85g05.s  
AA961445 or53e03.s

AI288030 qu99e04.x  
AI572314 te39f10.x  
AI630923 tz31h05.x  
AI758820 ty24h01.x  
AI800161 tr23b08.x  
AA446838 zw84h01.r  
AA568463 nm25d04.s  
BI753930 603022937  
BH644925 1M0804A41  
AZ600248 1M0418D11  
AI653845 ty02b12.x  
AL630583 1M0430583  
AI088727 qal6e11.x  
AI687864 qv07d12.x  
AI687937 tp99d01.x  
AZ330095 1M0214J19  
AZ833779 2M0116A09  
AZ608734 1M0433F11  
AZ641783 1M0504F06  
AZ655788 1M0537024  
AZ777445 2M0011C19  
AZ828747 2M0105J21  
AZ633504 1M0488K13  
AI039381 ox40c02.s  
AI560329 tn13a12.x  
AI194520 ty38c06.x  
AI689452 tx82e12.x  
AI813395 wk80g09.x  
BM400565 5009-0-75  
AZ371606 1M0123C07  
AZ456387 1M0259B21  
AZ623680 1M0459110  
AL463387 T. brucei  
AL463387 1M0269G05  
AZ465531 1M0275I02  
AZ594225 1M0406L01  
AZ697339 1M0570B15  
AL743393 Danilo rer  
AV832439  
BG642379 7b1 DrOSO  
AZ766046 1M0563M18  
AZ961620 2M0230B09  
AL497413 T. brucei  
AA836668 of53b11.s  
AA906611 ok79h09.s  
AI270065 qt91f01.x  
AI799261 tw55e03.x  
AI865809 wk86c07.x  
AA277392 vc10f05.r  
H27426 y144h02.r1  
AZ625604 1M0465D16  
AZ635438 1M0491J15  
AL759480 Arabidops  
AE64178 T. brucei  
BE396035 601312648  
AZ412343 1M0185E15  
AL768191 Arabidops  
BF533462 602074140  
AZ613697 1M0442K08  
AA873697 ob36g11.s  
AA938016 oo78f06.s  
AI200438 qf93b01.x  
AI475428 t183c09.x  
AI572876 tm63c03.x  
AI699754 tz12b01.x  
AI510857 vh55e05.r  
AV853613 AV853613  
BM008282 603617931  
AZ330770 1M0056M11  
AZ448522 1M0246F13  
AZ585763 1M0391K10  
AZ957024 2M0223E15  
AL462849 T. brucei

211	211	32	2,9	38	10	AV9600043	AV9600043	AV9600043	AV9600043	284	31	2,8	34	9	AI354356	qt74e01.x
c 212	c 212	32	2,9	38	13	BG912318	BG912318	602806861	602806861	c 285	31	2,8	34	9	AI370143	qu18h11.x
c 213	c 213	32	2,9	38	17	AZ34442	AZ34442	1M0078P20	1M0078P20	286	31	2,8	34	9	AA282064	xz02e01.s
c 214	c 214	32	2,9	38	17	AZ390541	AZ390541	1M0151021	1M0151021	287	31	2,8	34	13	BM398554	5009-0-47
c 215	c 215	32	2,9	38	17	AZ402445	AZ402445	1M0169D13	1M0169D13	288	31	2,8	34	14	N30949	yx50h03.r1
c 216	c 216	32	2,9	38	17	AZ490125	AZ490125	1M0322J19	1M0322J19	289	31	2,8	34	17	AZ309860	1M0017007
c 217	c 217	32	2,9	38	17	AZ588936	AZ588936	1M0397H05	1M0397H05	290	31	2,8	34	17	AZ377095	1M0131G14
c 218	c 218	32	2,9	38	17	AZ657455	AZ657455	1M0533H08	1M0533H08	c 291	31	2,8	35	9	AU260290	AU260290
c 219	c 219	32	2,9	38	17	AZ765843	AZ765843	1M0563E04	1M0563E04	c 292	31	2,8	35	13	BM398666	5009-0-48
c 220	c 220	32	2,9	38	17	AZ863994	AZ863994	2M0173B22	2M0173B22	c 293	31	2,8	35	17	AZ417100	1M0035E801
c 221	c 221	32	2,9	39	9	AL775941	AL775941	AL775941	AL775941	294	31	2,8	35	17	AZ403979	1M0035E801
c 222	c 222	32	2,9	39	12	BF344480	BF344480	602014879	602014879	295	31	2,8	35	17	AZ441999	1M0035E801
c 223	c 223	32	2,9	39	17	AQ2505109	AQ2505109	EP(3)0545	EP(3)0545	c 296	31	2,8	35	17	AZ843372	2M0142P10
c 224	c 224	32	2,9	39	17	AZ588176	AZ588176	1M0396M11	1M0396M11	c 297	31	2,8	35	17	AZ848745	2M0149E20
c 225	c 225	32	2,9	39	17	AZ657728	AZ657728	1M0533A908	1M0533A908	c 298	31	2,8	36	10	BE296967	BE296967
c 226	c 226	32	2,9	39	17	DR11A19T	DR11A19T	1M0533A908	1M0533A908	c 299	31	2,8	36	10	BE298656	601176480
c 227	c 227	32	2,9	40	9	AA872575	AA872575	ca16h08.s	ca16h08.s	300	31	2,8	36	13	BI861680	6033893356
c 228	c 228	32	2,9	40	9	AI089757	AI089757	qz22e03.x	qz22e03.x	c 301	31	2,8	37	9	AA701135	zg56e07.s
c 229	c 229	32	2,9	40	9	AI569502	AI569502	tw87h04.x	tw87h04.x	302	31	2,8	37	9	AI048978	uc77d09.y
c 230	c 230	32	2,9	40	9	AI609582	AI609582	tw28c02.x	tw28c02.x	303	31	2,8	37	9	AI475333	tl81h12.x
c 231	c 231	32	2,9	40	9	AI741783	AI741783	wg22h08.x	wg22h08.x	c 304	31	2,8	37	9	AI538439	ti06c05.x
c 232	c 232	32	2,9	40	9	AI745660	AI745660	tr24e02.x	tr24e02.x	c 305	31	2,8	37	9	AI625989	ar91h09.x
c 233	c 233	32	2,9	40	13	BE296536	BE296536	601174028	601174028	306	31	2,8	37	9	AA186584	zp64d06.r
c 234	c 234	32	2,9	40	13	BJ035979	BJ035979	BJ035979	BJ035979	c 307	31	2,8	37	10	AL682018	AL682018
c 235	c 235	32	2,9	40	13	BM398163	BM398163	5009-0-41	5009-0-41	308	31	2,8	37	10	AV966952	AV966952
c																

: 357	30	2.7	9	AA873288	oh68h09.s	C 430	30	2.7	37	9	AA902929	ok43f02t.s
358	30	2.7	25	AI298122	qm64e06.x	C 431	30	2.7	37	9	AI124999	ac12h07.s
359	30	2.7	25	AI664044	ue73e05.r	C 432	30	2.7	37	9	AI129902	qc41b07.x
360	30	2.7	25	AI6603284	AM0422E01	C 433	30	2.7	37	9	AI287459	qu99d07.x
361	30	2.7	25	AI6322343	IM0486K22	C 434	30	2.7	37	9	AI357088	qx16d03.x
362	30	2.7	25	IAZ872633	2M0186K01	C 435	30	2.7	37	9	AI499210	to08e02.x
363	30	2.7	25	BH812755	SALK_0630	C 436	30	2.7	37	9	AI582521	ts02a03.x
364	30	2.7	25	BH856288	SALK_0810	C 437	30	2.7	37	9	AI689454	tx94c06.x
365	30	2.7	25	AZ786827	2M0032N07	C 438	30	2.7	37	9	AI699754	tz12b01.x
366	30	2.7	26	BH814118	SALK_0657	C 439	30	2.7	37	9	AI755616	EFEStea38
367	30	2.7	26	TA381C07Q	T_ brucei	C 440	30	2.7	37	9	AI796585	wh58b02.x
368	30	2.7	27	AZ768008	IM0567D14	C 441	30	2.7	37	9	AL677081	AL677081
369	30	2.7	27	AZ782899	2M0024H09	C 442	30	2.7	37	17	AZ448522	IM0246FL3
370	30	2.7	27	TA21D032	T. brucei	C 443	30	2.7	37	17	AZ785556	2M0029G05
371	30	2.7	28	AI174332	anl7d02.s	C 444	30	2.7	37	17	AZ836826	2M0131A20
372	30	2.7	28	AI416657	sal0b04.x	C 445	30	2.7	37	17	AL497132	T. brucei
373	30	2.7	28	AI1916689	ta89f07.x	C 446	30	2.7	38	13	BI085006	602869S12
374	30	2.7	28	AZ343801	IM0077B04	C 447	30	2.7	38	13	BM399387	5009-0-57
375	30	2.7	28	AZ489682	IM0322G16	C 448	30	2.7	38	17	AZ304825	IM0005O15
376	30	2.7	29	AZ830543	2M0109P18	C 449	30	2.7	38	17	AZ309141	IM0012P21
377	30	2.7	31	AA876793	nz48e12.s	C 450	30	2.7	38	17	AZ351594	IM0089A15
378	30	2.7	31	AA878818	of83d05.s	C 451	30	2.7	38	17	AZ495773	IM0331O13
379	30	2.7	31	AI000997	os45h09.s	C 452	30	2.7	38	17	AZ768399	IM0568E19
380	30	2.7	31	AI299061	qn35f01.x	C 453	30	2.7	39	10	BE617821	601441869
381	30	2.7	31	AI560711	t655e02.x	C 454	30	2.7	39	13	BM396197	5009-0-18
382	30	2.7	31	BI5986603	603231351	C 455	30	2.7	39	13	BM396197	5009-0-18
383	30	2.7	32	AU259040	AU259040	C 456	30	2.7	39	17	AZ402785	IM0170E14
384	30	2.7	32	BM398164	5009-0-41	C 457	30	2.7	39	17	AZ459707	IM0264B18
385	30	2.7	32	AZ308819	IM0012P08	C 458	30	2.7	39	17	AZ804350	2M0065M24
386	30	2.7	32	AZ861976	2M0169H04	C 459	30	2.7	39	17	AZ946943	2M0208P22
387	30	2.7	32	AV832439	AV832439	C 460	30	2.7	39	17	AZ986277	2M0268J20
388	30	2.7	32	BG820103	602782312	C 461	30	2.7	39	17	AL762782	Arabidops
389	30	2.7	32	BF346872	BF346872	C 462	30	2.7	39	17	TA122GG01P	AL462659 T. brucei
390	30	2.7	33	N40522	yw75hl2.rl	C 463	30	2.7	40	9	AA873888	



## ALIGNMENTS

RESULT 1  
AA999756/c 31 bp mRNA linear EST 05-JUN-1998  
LOCUS OS99e04.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1612926 3',  
DEFINITION similar to TR:062084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;, mRNA  
sequence.  
ACCESSION AA999756  
VERSION AA999756.1 GI:3190311  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

## FEATURES

source  
1..31  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1612926"  
/clone\_lib="NCI\_CGAP\_GC3"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT73  
vector. Library is not normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

3 a 11 c 16 g 1 t

## ALIGNMENT Scores:

Pred. No.: 1.09e+05 Length: 31  
Score: 44.00 Matches: 7  
Percent Similarity: 88.8% Conservative: 1  
Best Local Similarity: 77.7% Mismatches: 1  
Query Match: 3.9% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA999756 (1-31)

QY 39 ProProGlyAlaAlaProAlaProGly 47  
||||||| :|||||||  
Db 30 CGCGCCGACCTCTCTCTCGCCCGGG 4

## RESULT 2

AA1811024 34 bp mRNA linear EST 07-JUL-1999  
LOCUS tr03a03.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217196 3',  
DEFINITION similar to TR:P92327 P92327 PROLINE-RICH PROTEIN PRP2 PRECURSOR.  
; contains element MSK1 repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA1811024 1 GI:5397590  
EST.  
human.  
Homo sapiens

REFERENCE 1 (bases 1 to 34)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

## FEATURES

source  
1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2217196"  
/clone\_lib="NCI\_CGAP\_Ov23"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.35 kb. Tumor types include: mixed  
Mullerian tumor, papillary serous, clear cell, spindle  
cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"

## BASE COUNT

10 a 17 c 6 g 1 t

## ALIGNMENT Scores:

Pred. No.: 1.77e+05 Length: 34  
Score: 42.00 Matches: 7  
Percent Similarity: 77.7% Conservative: 0  
Best Local Similarity: 77.7% Mismatches: 2  
Query Match: 3.8% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA1811024 (1-34)

QY 39 ProProGlyAlaAlaProAlaProGly 47  
||||||| ||||| |||||  
Db 4 CCCCCGGAAGAGCCGCCCGCGGA 30

## RESULT 3

AA1698327/c 37 bp mRNA linear EST 16-DEC-1999  
LOCUS tx63c12.x1 NCI\_CGAP\_Utl1 Homo sapiens cDNA clone IMAGE:2274262 3',  
DEFINITION similar to TR:Q41120 Q41120 HYDROXYPROLINE-RICH GLYCOPROTEIN ;,  
mRNA sequence.

AA1698327 37 bp mRNA linear EST 16-DEC-1999  
VERSION AA1698327.1 GI:4986227  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1039 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1. 37  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2274262"  
/clone\_lib="NCI-CGAP\_Utl"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI;  
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

BASE COUNT 9 a 7 c 21 g 0 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1.94e+05 Length: 37  
Score: 42.00 Matches: 7  
Percent Similarity: 72.73% Conservative: 1  
Best Local Similarity: 63.64% Mismatches: 3  
Query Match: 3.80% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AT698327 (1-37)

Qy 39 ProProGlyAlaAlaProAlaProGlyIlePhe 49  
|||||  
Db 37 CCCCCGGGGCCCCCCCCCTCCCGCTGTTT 5

RESULT 4  
AI202980

LOCUS q32e08.x1 NCI-CGAP\_GC6 Homo sapiens CDNA clone IMAGE:1942598 3'  
DEFINITION similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L  
; contains element MSRL repetitive element ;, mRNA sequence.

ACCESSION AI202980.1 GI:3755586  
VERSION AI202980  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 34)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index

## AUTHORS

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

## JOURNAL

COMMENT Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center

FEATURES  
source

1. 34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1942598"  
/clone\_lib="NCI-CGAP\_GC6"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pW7T3D-Pac (Pharmacia) with a modified  
polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA  
from the normalized library NCI-CGAP\_GC4 was prepared, and  
ss circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 3 a 22 c 9 g 0 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2.14e+05 Length: 34  
Score: 41.00 Matches: 7  
Percent Similarity: 63.64% Conservative: 0  
Best Local Similarity: 63.64% Mismatches: 4  
Query Match: 3.71% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI202980 (1-34)

Qy 36 GlyAlaAlaProProGlyAlaAlaProAlaPro 46  
|||  
Db 1 GGGGGCCCCCCCCAGGCGAAGCCCCCCCCCCC 33

RESULT 5  
AI628006/c

LOCUS AI628006 40 bp mRNA linear EST 07-MAR-2000  
DEFINITION ty21d06.x1 NCI-CGAP\_Ut3 Homo sapiens CDNA clone IMAGE:2279723 3'  
similar to TR:Q43687 Q43687 EXTENSIN-LIKE PROTEIN ; contains element  
MSRL repetitive element ;, mRNA sequence.

ACCESSION AI628006  
VERSION AI628006.1 GI:4664806  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 40)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

## JOURNAL

COMMENT Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Greg Lennon, Ph.D.  
CDNA Library Arrayed by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1838 Std Error: 0.00  
Seq primer: -40UP from Gibco

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

High quality sequence stop: 1  
POLYA=No.

# FEATURES

source

Location/Qualifiers  
1. 40  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:229723"  
/clone\_lib="NCI\_CGAP\_Ut3"  
/tissue\_type="poorly differentiated endometrial  
adenocarcinoma, 2 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.45 kb. Life Technologies catalog #:  
11541-018"

BASE COUNT 8 a 11 c 18 g 3 t

ORIGIN

## Alignment Scores:

Red. No.: 2.56e+05 Length: 40  
Score: 41.00 Matches: 7  
Percent Similarity: 61.54% Conservative: 1  
Best Local Similarity: 53.85% Mismatches: 5  
Query Match: 3.71% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AF628006 (1-40)

QY 41 GlyAlaAlaProAlaProGlyIlePheSerSerGlnPro 53

DB 40 GGGGGCCCCAGACCCGGGTGTTCCTCTCCCT 2

## RESULT 6

AI422710/c

LOCUS

DEFINITION

AI422710 31 bp mRNA linear EST 30-MAR-1999  
tf29d12.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2097623 3'  
similar to SW:CAL3\_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.  
; contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AI422710

VERSION AI422710.1 GI:4268641

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

COMMENT (CGAP/RTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 616 Std Error: 0.00

Seq primer: -40bp from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 31

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2097623"

/clone\_lib="NCI\_CGAP\_Brn23"

## FEATURES

source

/tissue\_type="glioblastoma (pooled)"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGGCATATCTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 3 a 12 c 15 g 1 t

ORIGIN

## Alignment Scores:

Red. No.: 2.33e+05 Length: 31  
Score: 40.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI422710 (1-31)

QY 39 ProProGlyAlaAlaProAlaProGly 47

DB 30 CCCCCGGGGCCCCCTTGGCCGGG 4

## RESULT 7

BM010450/c

LOCUS

DEFINITION

BM010450 36 bp mRNA linear EST 30-OCT-2001  
603631395F1 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5445310 5',  
mRNA sequence.

ACCESSION BM010450

VERSION BM010450.1 GI:16524804

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1925 row: m column: 23

High quality sequence stop: 36.

Location/Qualifiers

1. 36

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5445310"

/clone\_lib="NIH\_MGC\_41"

/tissue\_type="amelanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH\_MGC Library."

BASE COUNT 7 a 11 c 16 g 2 t

ORIGIN

Alignment Scores:		2.76e+05	Length:	36
Pred. No.:		40.00	Matches:	7
Score:		75.00%	Conservative:	2
Best Local Similarity:		58.33%	Mismatches:	3
Query Match:		3.62%	Indels:	0
DB:		13	Gaps:	0
US-09-375-514-22 (1-205) x BM010450 (1-36)				
Qy	35	ValGlyAlaAProProGlyAlaAProAlaPro 46		
Db	36	ATGGGGCGTCCCTCAGGCGCTGCTCCTCTCCC 1		
RESULT 8				
BM010792/c				
LOCUS				
DEFINITION				
603629306F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434872 5',				
mRNA sequence.				
BM010792				
BM010792.1 GI:16525146				
EST.				
SOURCE				
human.				
ORGANISM				
Homo sapiens				
REFERENCE				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
1 (bases 1 to 36)				
NIH-MGC http://mgi.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
JOURNAL				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-r@mail.nih.gov				
Tissue Procurement: DCTD/DP				
cDNA Library Preparation: Ling Hong/Rubin Laboratory				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LNL at:				
http://image.llnl.gov				
Plate: LCM1912 row: k column: 01				
High quality sequence stop: 36.				
FEATURES				
Location/Qualifiers				
1..36				
/organism="Homo sapiens"				
/db_xref="taxon:9606"				
/clone="IMAGE:5434872"				
/clone_lib="NIH_MGC_41"				
/tissue_type="amelanotic melanoma, cell line"				
/lab_host="DH10B (phage-resistant)"				
/note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:				
EcoRI; cDNA made by oligo-dr priming. Directionally cloned				
into EcoRI/XhoI sites using the following 5' adaptor:				
GGCAGGAG(G). Library constructed by Ling Hong in the				
Laboratory of Gerald M. Rubin (University of California,				
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and				
Superscript II RT (Life Technologies). Note: this is a				
NIH_MGC Library."				
7 a 11 c 16 g 2 t				
BASE COUNT				
ORIGIN				
Alignment Scores:				
Pred. No.:		2.76e+05	Length:	36
Score:		40.00	Matches:	7
Percent Similarity:		75.00%	Conservative:	2
Best Local Similarity:		58.33%	Mismatches:	3
Query Match:		3.62%	Indels:	0
DB:		13	Gaps:	0
US-09-375-514-22 (1-205) x BM010792 (1-36)				
Qy	35	ValGlyAlaAProProGlyAlaAProAlaPro 46		
Db	36	ATGGGGCGTCCCTCAGGCGCTGCTCCTCTCCC 1		
RESULT 9				
AI683252				
LOCUS				
DEFINITION				
tx02612.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2268046 3',				
similar to TR:Q04118 Q04118 SALIVARY PROLINE-RICH GLYCOPROTEIN G1				
PRECURSOR. ;contains TARI.b2 MSRI repetitive element ;, mRNA				
sequence.				
AI683252				
AI683252.1 GI:4893434				
EST.				
SOURCE				
human.				
ORGANISM				
Homo sapiens				
REFERENCE				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
1 (bases 1 to 37)				
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
Tumor Gene Index				
Unpublished (1997)				
JOURNAL				
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs-r@mail.nih.gov				
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.				
Emmert-Buck, M.D., Ph.D.				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed by: Greg Lennon, Ph.D.				
DNA Sequencing by: Washington University Genome Sequencing Center				
Clone distribution: NCI-CGAP clone distribution information can be				
found through the I.M.A.G.E. Consortium/LNL at:				
www.bio.llnl.gov/bbrp/image/image.html				
Trace considered overall poor quality				
Insert Length: 874 Std Error: 0.00				
Seq primer: -400P from Gibco				
High quality sequence stop: 1.				
FEATURES				
Location/Qualifiers				
1..37				
/organism="Homo sapiens"				
/db_xref="taxon:9606"				
/clone="IMAGE:2268046"				
/clone_lib="NCI_CGAP_Ut4"				
/tissue_type="serous papillary carcinoma, high grade, 2				
pooled tumors"				
/lab_host="DH10B"				
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;				
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.				
Average insert size 1.48 kb. Life Technologies catalog #:				
11542-016"				
BASE COUNT				
ORIGIN				
Alignment Scores:				
Pred. No.:		2.84e+05	Length:	37
Score:		40.00	Matches:	7
Percent Similarity:		70.00%	Conservative:	0
Best Local Similarity:		70.00%	Mismatches:	3
Query Match:		3.62%	Indels:	0
DB:		9	Gaps:	0
US-09-375-514-22 (1-205) x AI683252 (1-37)				
Qy	75	ProAlaAProGlyAlaAProAlaAPro 84		
Db	7	CCCCAGGCGCGGGGGGGCCACAGGGCCC 36		
RESULT 10				
HSM003700				
ID				
HSM003700 standard; RNA; EST; 40 BP.				
XX				
AL039224;				
XX				
AL039224.1				
SV				

XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 DE Homo sapiens mRNA; EST DKFZp(null)E191\_r1 (from clone DKFZp(null)E191)  
 XX EST; expressed sequence tag.  
 KW Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX [1]  
 RN 1-40  
 RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX Clon from S. Wiemann, sequenced by DKFZ within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No s1 sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6; 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX Key Location/Qualifiers  
 FH 1. 40  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp(null)E191"  
 FT /clone\_lib="(null) (synonym: hmcfl). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="breast cancer"  
 XX Sequence 40 BP; 6 A; 16 C; 9 G; 9 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.1e+05 Length: 40  
 Score: 40.00 Matches: 6  
 Percent Similarity: 88.89% Conservative: 2  
 Best Local Similarity: 66.67% Mismatches: 1  
 Query Match: 3.62% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-375-514-22 (1-205) x HSM003700 (1-40)  
 DY 86 LeuSerProValProValValHis 94  
 DB 4 ATGTCCCTGTGTCACCACTCTGCAC 30  
 RESULT 11  
 AZ782295 27 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0022019F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGC2M0022019 F, DNA sequence.  
 ACCESSION AZ782295  
 VERSION AZ782295.1 GI:12915874  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 TITLE  
 JOURNAL

COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0022 row: 0 column: 19  
 Seq primer: CCGTGTAAACGACGAGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 1. .27  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0022019"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 4 a 3 c 12 g 8 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.42e+05 Length: 27  
 Score: 39.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1  
 Query Match: 3.53% Indels: 0  
 DB: 17 Gaps: 0  
 US-09-375-514-22 (1-205) x AZ782295 (1-27)  
 QY 55 HisThrProHisProAlaAlaSer 62  
 DB 24 CACACCCACATCCAGAGGCCACA 1  
 RESULT 12  
 BE729288/c  
 LOCUS BE729288  
 DEFINITION BE729288 Homo sapiens  
 mRNA sequence.  
 ACCESSION BE729288  
 VERSION BE729288.1 GI:10143280  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 34)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 REFERENCE  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L1CM506 row: j column: 14.  
Location/Qualifiers

## FEATURES

source

1. .34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3831277"  
/clone\_lib="NIH\_MGC\_20"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 8 a 5 c 15 g 6 t  
ORIGIN

## Alignment Scores:

Pred. No.: 3.13e+05 Length: 34  
Score: 39.00 Matches: 6  
Percent Similarity: 88.89% Conservative: 2  
Best Local Similarity: 66.67% Mismatches: 1  
Query Match: 3.53% Indels: 0  
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x BE729288 (1-34)

QY 38 AlapProGlyAlaAlaProAlaPro 46

Db 34 TCACCACCGGGCTCGACCTAGCCCT 8

## RESULT 13

AI912532/c

LOCUS

DEFINITION t225q07.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2289660 3' similar to TR:056971 056971 ORF FOR OVERLAPPING PROTEIN. ; contains MER22.b2 MSRI repetitive element ; , mRNA sequence.

## ACCESSION

AI912532

VERSION AI912532.1 GI:5632387

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 31)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1799 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

## FEATURES

source

Location/Qualifiers  
1. .31  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2289660"  
/clone\_lib="NCI CGAP Ut2"  
/tissue\_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.85 kb. Life Technologies catalog #:  
11539-012"

BASE COUNT 6 a 22 c 0 g 3 t  
ORIGIN

## Alignment Scores:

Pred. No.: 3.4e+05 Length: 31  
Score: 38.00 Matches: 5  
Percent Similarity: 85.71% Conservative: 1  
Best Local Similarity: 71.43% Mismatches: 1  
Query Match: 3.44% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI912532 (1-31)

QY 191 AspAsnGlyGlyTrpValGly 197

Db 30 GATGGGGGGGGTGGATTGGG 10

## RESULT 14

AI131930

LOCUS

DEFINITION uc33q07.x1 Soares\_mammary\_gland\_NbMWG Mus musculus cDNA clone IMAGE:1399836 5' similar to TR:035034 035034 CPE-RECEPTOR. ; , mRNA sequence.

ACCESSION AI131930

VERSION AI131930.1 GI:3601946

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 34)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:911552

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .34

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

FEATURES

source

Location/Qualifiers

1. .34

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

Trace considered overall poor quality

/clone="IMAGE:1399836"  
 /clone\_lib="Soares\_mammary\_gland\_NbMMG"  
 /sex="male"  
 /tissue\_type="mammary gland"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"

/note="organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia RI; 1st strand cDNA was primed with a Not I - oIIgo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 3 a 13 c 10 g 8 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3.76e+05 Length: 34  
 Score: 38.00 Matches: 7  
 Percent Similarity: 88.89% Conservative: 1  
 Best Local Similarity: 77.78% Mismatches: 1  
 Query Match: 3.44% Indels: 0  
 DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AII131930 (1-34)

QY 43 AlaProAlaProGlyIlePheSerSer 51

DB 4 GCTCAGCTCTGGGCTACTGTCTAGC 30

RESULT 15

AZ832681

LOCUS

DEFINITION

2M0113H24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0113H24 F, DNA sequence.

ACCESSION

AZ832681

VERSION

AZ832681.1 GI:13002685

KEYWORDS

GSS.

SOURCE

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0113 row: H column: 24

Seq primer: CGTTGTAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 35.

Location/Qualifiers

1..35

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0113H24"

FEATURES

source

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 2 c 20 g 7 t  
 ORIGIN

Alignment Scores:

Pred. No.: 3.89e+05 Length: 35  
 Score: 38.00 Matches: 6  
 Percent Similarity: 77.78% Conservative: 1  
 Best Local Similarity: 66.67% Mismatches: 2  
 Query Match: 3.44% Indels: 0  
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ832681 (1-35)

QY 192 AsnGlyGlyTrpValGlyAlaSerGly 200

DB 4 AATCGCGGTGGATGGAGTGGTGG 30

RESULT 16

BE395744

LOCUS

DEFINITION

601311259F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3632655 5',

mrna sequence.

ACCESSION

BE395744

VERSION

BE395744.1 GI:9341109

KEYWORDS

EST.

SOURCE

human.

ORGANISM

REFERENCE

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CNA Library Preparation: Ling Hong/Rubin Laboratory

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC324 row: f column: 16

High quality sequence stop: 36.

Location/Qualifiers

1..36

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3632655"

/clone\_lib="NIH\_MGC\_44"

/tissue\_type="endometrium, adenocarcinoma cell line"



/lab\_host="DH10B (phage-resistant)"  
 /note="organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACAGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 7 a 9 c 10 g 10 t  
 ORIGIN

Alignment Scores: 4.01e+05 Length: 36  
 Pred. No.: 38.00 Matches: 6  
 Score: 83.3% Conservative: 4  
 Percent Similarity: 50.0% Mismatches: 2  
 Best Local Similarity: 3.44% Indels: 0  
 Query Match: 10 Gaps: 0  
 DB:

US-09-375-514-22 (1-205) x BE395744 (1-36)

Qy 11 AsnArgGluIleValMetIleHisTyrLys 22  
 |||||:::||||: ::::: |||||  
 Db 1 AACCGGAGCTGTGTTGACCTTCCTCTACAAG 36

RESULT 17  
 AZ580135/c 37 bp DNA linear GSS 13-DEC-2000  
 LOCUS  
 DEFINITION 1M0368E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0368E16 F, DNA sequence.

ACCESSION AZ580135  
 VERSION AZ580135.1 GI:11694564  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0368 row: E column: 16  
 Seq primer: CTTGTAAACGACGGCCAGT

Class: plasmid ends  
 High quality sequence stop: 37.  
 Location/Qualifiers  
 1. .37  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0368E16"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gii4732114|gbiAF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 20 g  
 ORIGIN

Alignment Scores: 4.14e+05 Length: 37  
 Pred. No.: 38.00 Matches: 7  
 Score: 63.64% Conservative: 0  
 Percent Similarity: 63.64% Mismatches: 4  
 Best Local Similarity: 3.44% Indels: 0  
 Query Match: 17 Gaps: 0  
 DB:

US-09-375-514-22 (1-205) x AZ580135 (1-37)

Qy 53 ProGlyHisThrProHisProAlaAlaSerArg 63  
 ||| ||||| ||||| |||||  
 Db 37 CCTGCCCTGCCCTCACCTGCCGCTCGCGA 5

RESULT 18  
 BG709439/c 40 bp mRNA linear EST 07-MAY-2001  
 LOCUS  
 DEFINITION 602673496F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4796398 5',  
 mRNA sequence.

ACCESSION BG709439  
 VERSION BG709439.1 GI:13987776  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT NTH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 40)  
 NTH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM10680 row: 0 column: 23  
 High quality sequence stop: 40.  
 Location/Qualifiers  
 1. .40

FEATURES  
 source

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4796398"  
 /clone\_lib="NIH\_MGC\_96"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',  
 size-selected for average insert size 2.3 kb and  
 normalized to ROT 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

# BASE COUNT

5 a 15 c 15 g 5 t

# ORIGIN

## Alignment Scores:

Pred. No.: 4.51e+05 Length: 40  
Score: 38.00 Matches: 8  
Percent Similarity: 72.73% Conservative: 0  
Best Local Similarity: 72.73% Mismatches: 3  
Query Match: 3.44% Indels: 0  
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x BG709439 (1-40)

QY 75 ProAlaAProGlyAlaAlaGlyProAla 85

DB 33 CGAAGGCGACGGCTGCAGCGGGGACCCGCT 1

## RESULT 19

AZ780387

LOCUS

DEFINITION 29 bp DNA linear GSS 16-FEB-2001  
clone UUGC2M0017N12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ780387

VERSION A2780387.1 GI:12911997

KEYWORDS GSS.

SOURCE house mouse.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 29)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

## TITLE

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: N column: 12  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

## FEATURES

Location/Qualifiers

1..29  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0017N12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 23 g 5 t

# ORIGIN

## Alignment Scores:

Pred. No.: 3.81e+05 Length: 29  
Score: 37.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.35% Indels: 0  
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ780387 (1-29)

QY 194 GlyTTPValGlyAlaSerGly 200

DB 3 GGGTGGTGGGGGGGAGTGGG 23

## RESULT 20

AZ784258/c

LOCUS

DEFINITION 33 bp DNA linear GSS 16-FEB-2001  
clone UUGC2M0026G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ784258

VERSION A2784258.1 GI:12919799

KEYWORDS GSS.

SOURCE house mouse.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 33)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

## TITLE

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0026 row: G column: 22  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 33.

## FEATURES

Location/Qualifiers

1..33  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0026G22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (91473211419b1AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 7 c 16 g 8 t

## ORIGIN

## Alignment Scores:

Pred. No.: 4.4e+05 Length: 33  
Score: 37.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 1  
Best Local Similarity: 83.33% Mismatches: 0  
Query Match: 3.35% Indels: 0  
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ784258 (1-33)

Qy 54 GlyHisThrProHisPro 59

Db 25 GGGCACTGGCCGCCACCCC 8

## RESULT 21

## LOCUS

AI217993 34 bp mRNA linear EST 10-NOV-1998  
q52910.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1753698  
3' similar to SW:CALL\_MOUSE P11087 PROCOLLAGEN ALPHA 1(I) CHAIN  
PRECURSOR. ; contains MER22.b3 MSRI MSRI repetitive element ; , mRNA  
sequence.

## ACCESSION

VERSION AI217993.1 GI:3797808

## KEYWORDS

EST.

## SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

## JOURNAL

COMMENT

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 826 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

## FEATURES

source

1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1753698"  
/sex="male"  
/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 11 c 18 g 3 t

## ORIGIN

## Alignment Scores:

Pred. No.: 4.55e+05 Length: 34  
Score: 37.00 Matches: 6  
Percent Similarity: 66.67% Conservatives: 0  
Best Local Similarity: 66.67% Mismatches: 3  
Query Match: 3.35% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI217993 (1-34)

Qy 39 ProProGlyAlaAlaProAlaProGly 47

Db 31 CGCGCGGGCGCCGCCCGCGCGCTGGT 5

## RESULT 22

## LOCUS

AI362411 34 bp mRNA linear EST 06-JAN-1999  
qV92602.x1 NCI-CGAP\_Ut2 Homo sapiens cDNA clone IMAGE:1989050 3'  
similar to SW:CALL\_RAT P02454 COLLAGEN ALPHA 1(I) CHAIN ; contains  
element MER22 repetitive element ; , mRNA sequence.

## ACCESSION

VERSION AI362411.1 GI:4114032

## KEYWORDS

EST.

## SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmett-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

## FEATURES

source

1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1989050"  
/clone\_lib="NCI-CGAP\_Ut2"  
/tissue\_type="moderately-differentiated endometrial  
adenocarcinoma, 3 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.85 kb. Life Technologies catalog #:  
11539-012"

BASE COUNT 0 a 15 c 18 g 1 t

## ORIGIN

## Alignment Scores:

Pred. No.: 4.55e+05 Length: 34  
Score: 37.00 Matches: 6



ACCESSION AI015468  
 VERSION AI015468.1 GI:3229804  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 40)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

## TITLE

Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 500 Std Error: 0.00

Seq primer: -40m13 fwd. Et from Amersham

High quality sequence stop: 1.

## FEATURES

Location/Qualifiers

1..40

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1641164"

/clone\_lib="Soares\_testis\_NHT"

/sex="male"

/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech Laboratories  
 , Inc., and primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGGAGCGGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

ORIGIN

4 a 13 c 16 g 7 t

## Alignment Scores:

Pred. No.: 5,45e+05 Length: 40

Score: 37.00 Matches: 7

Percent Similarity: 58.33% Conservative: 0

Best Local Similarity: 58.33% Mismatches: 5

Query Match: 3.35% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI015468 (1-40)

Qy 35 ValGlyAlaProGlyAlaProGlyAlaProAlaPro 46

Db 1 GTGGCGCGTTCGCCGACGCTCCAGACCTTGCGC 36

## RESULT 26

AI800161

LOCUS

tr23b08.x1 NCI-CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2219127 3'

similar to SW:CA13\_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.

; contains element MSRI repetitive element ; mRNA sequence.

## ACCESSION

AI800161

VERSION

AI800161.1 GI:5365633

KEYWORDS

EST.

SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

## FEATURES

Location/Qualifiers

1..40

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2219127"

/clone\_lib="NCI-CGAP\_Ov23"

/tissue\_type="tumor, 5 pooled (see description)"

/lab\_host="DH10B"

/note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: SalI;

Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.35 kb. Tumor types include: mixed

Mullerian tumor, papillary serous, clear cell, spindle

cell. All are primary tumors, metastasis positive. Life

Technologies catalog #: 11534-013"

BASE COUNT 1 a 23 c 14 g 1 t

ORIGIN

## Alignment Scores:

Pred. No.: 5,45e+05 Length: 40

Score: 37.00 Matches: 7

Percent Similarity: 66.67% Conservative: 1

Best Local Similarity: 58.33% Mismatches: 4

Query Match: 3.35% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI800161 (1-40)

Qy 54 GlyHisThrProHisProAlaAlaSerArgAspPro 65

Db 1 GGGCCCTCCCCCCCCCGGGCGCCCGGGGACCG 36

## RESULT 27

AZ982483

LOCUS

2M0263K16F Mouse 10kb plasmid UUCG2M library Mus musculus genomic

clone UUCG2M0263K16 F, DNA sequence.

DEFINITION

ACCESSION

VERSION

AZ982483.1 GI:13853710

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0263 Row: K Column: 16  
 Seq primer: CGTTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.

## FEATURES

source

1. 24  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0263K16"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 17 g 4 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 3.73e+05 Length: 24  
 Score: 36.00 Matches: 6  
 Percent Similarity: 85.71% Conservative: 0  
 Best Local Similarity: 85.71% Mismatches: 1  
 Query Match: 3.26% Indels: 0  
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ982483 (1-24)

QY 194 GlyTnpValGlyAlaSerGly 200

Db 1 GGGTGGGTAGGGAGCTGTGG 21  
 |||||

RESULT 28

AW250272/c

LOCUS

DEFINITION

AW250272

AW250272.1 GI:6593265

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

2821187.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821187 5',  
 mRNA sequence.

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

27 bp linear EST 07-JAN-2000

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 9 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 27 contiguous distinct peaks

following vector sequence.

Plate: LUCM6 row: C column: 12

High quality sequence stop: 9.

1. 27

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2821187"

/clone\_lib="NIH\_MGC\_7"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life technologies)."

BASE COUNT 2 a 7 c 15 g 3 t

ORIGIN

Alignment Scores:

Pred. No.: 4.25e+05 Length: 27

Score: 36.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 3.26% Indels: 0

DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x AW250272 (1-27)

QY 54 GlyHisThrProHisProAlaAla 61

||| |||||

Db 24 GCGCGCACACGCGACCTCGTGCC 1

RESULT 29

AA871994/c

LOCUS

DEFINITION

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA871994.1 GI:2968032

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871994

AA





/note="Organ: pancreas; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT 3 a 16 c 10 g 2 t  
ORIGIN

## Alignment Scores:

Pred. No.: 4.96e+05 Length: 31  
Score: 36.00 Matches: 6  
Percent Similarity: 66.67% Conservative: 0  
Best Local Similarity: 66.67% Mismatches: 3  
Query Match: 3.26% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AT677781 (1-31)

QY 34 AspValGlyAlaAlaProGlyAla 42

Db 27 GACGCGGGGGTGTCCCGCGGGCGG 1

## RESULT 32

BI762555/c

LOCUS BI762555 32 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603048685F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5188724 5',

## ACCESSION

BI762555

VERSION BI762555.1 GI:15754133

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 32)

NIH-MGC http://mgc.nci.nih.gov/

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11471 row: j column: 21

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5188724"

/lab\_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:

pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH\_MGC Library."

BASE COUNT 12 a 4 c 15 g 1 t

## ORIGIN

Alignment Scores:

Pred. No.: 5.14e+05 Length: 32

Score: 36.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI762555 (1-32)

QY 84 ProAlaLeuSerProValPro 91

Db 30 CCGCTCTGTCTCCGCTGCCTCCA 7

RESULT 33

BI832949/c

LOCUS BI832949 32 bp mRNA linear EST 04-OCT-2001

DEFINITION 603090781F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5229596 5',

BI832949

VERSION BI832949.1 GI:15944499

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 32)

NIH-MGC http://mgc.nci.nih.gov/

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11578 row: a column: 21

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5229596"

/lab\_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector:

pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA

source anonymous pool of spleen and pancreas from 28 yo

male. Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.5 kb, insert size range 1-2.5 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 025. Note: this is a NIH\_MGC Library."

BASE COUNT 12 a 4 c 15 g 1 t

## ORIGIN

Alignment Scores:

Pred. No.: 5.14e+05 Length: 32

Score: 36.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.26% Indels: 0

DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI832949 (1-32)

QY 84 ProAlaLeuSerProValPro 91

Db 30 CCGCTCTGTCTCCGCTGCCTCCA 7

RESULT 34

BI833158/c

LOCUS BI833158 32 bp mRNA linear EST 04-OCT-2001

```

DEFINITION 60309081F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229597 5',
            mRNA sequence.
ACCESSION  BI833158
VERSION    BI833158.1  GI:15944708
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 32)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1578 row: a column: 22
            High quality sequence stop: 32.
FEATURES   Location/Qualifiers
            1..32
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5229597"
            /clone_lib="NIH_MGC_120"
            /lab_host="DH10B"
            /note="Organ: pooled pancreas and spleen; Vector:
            pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
            source anonymous pool of spleen and pancreas from 28 yo
            male. Library is oligo-dT primed and directionally cloned
            (EcoRV site is destroyed upon cloning). Average insert
            size 1.5 kb, insert size range 1-2.5 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT  12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833158 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCCTCCA 7
RESULT 35
BI833514/c
LOCUS 32 bp mRNA linear EST 04-OCT-2001
DEFINITION 603088181F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5226933 5',
            mRNA sequence.
ACCESSION  BI833514
VERSION    BI833514.1  GI:15945064
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 32)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)

```

```

COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1571 row: b column: 22
            High quality sequence stop: 32.
FEATURES   Location/Qualifiers
            1..32
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5226933"
            /clone_lib="NIH_MGC_120"
            /lab_host="DH10B"
            /note="Organ: pooled pancreas and spleen; Vector:
            pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
            source anonymous pool of spleen and pancreas from 28 yo
            male. Library is oligo-dT primed and directionally cloned
            (EcoRV site is destroyed upon cloning). Average insert
            size 1.5 kb, insert size range 1-2.5 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT  12 a 4 c 15 g 1 t
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+05 Length: 32
Score: 36.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.26% Indels: 0
DB: 13 Gaps: 0
US-09-375-514-22 (1-205) x BI833514 (1-32)
QY 84 ProAlaLeuSerProValPro 91
Db 30 CCGCTCTCTCTCCGCTGCCTCCA 7
RESULT 36
AZ320746/c
LOCUS 32 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0040P21R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
            clone UUGCLM0040P21 R, DNA sequence.
ACCESSION  AZ320746
VERSION    AZ320746.1  GI:10372836
KEYWORDS  GSS.
SOURCE    house mouse.
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 32)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00

```

Plate: 0040 row: P column: 21  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 32.  
 Location/Qualifiers

# FEATURES

source

1. 32  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0040P21"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114|g114732114|g114732114), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 7 c 12 g 7 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 5.14e+05 Length: 32  
 Score: 36.00 Matches: 6  
 Percent Similarity: 60.00% Conservative: 0  
 Best Local Similarity: 60.00% Mismatches: 4  
 Query Match: 3.26% Indels: 0  
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ320746 (1-32)

QY 54 GlyHisThrProHisProAlaSerArg 63  
 ||| ||||| ||||| |||||  
 Db 31 GGGCAACTCCCTCATCCACAGGATCGGA 2

## RESULT 37

BI829654/c

LOCUS

DEFINITION BI829654 33 bp mRNA linear EST 04-OCT-2001  
 mRNA sequence.

ACCESSION BI829654

VERSION BI829654.1 GI:15941204

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: LLAM1425 row: P column: 24  
 High quality sequence stop: 33.  
 Location/Qualifiers

# FEATURES

source

1. 33  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5171207"  
 /clone\_lib="NIH\_MGC\_119"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

BASE COUNT 12 a 4 c 16 g 1 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 5.32e+05 Length: 33  
 Score: 36.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1  
 Query Match: 3.26% Indels: 0  
 DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI829654 (1-33)

QY 84 ProAlaLeuSerProValProPro 91  
 ||| ||||| ||||| |||||

Db 31 CCGCCTCTGTCGCTCGCTGCCA 8

## RESULT 38

LOCUS AI589397

DEFINITION

AI589397 34 bp mRNA linear EST 21-APR-1999  
 tr61h11.x2 NCI-CGAP\_Panl Homo sapiens cDNA clone IMAGE:2222853 3'  
 similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RPL15  
 PRECURSOR. ; contains element MSRL repetitive element ; , mRNA  
 sequence.

ACCESSION AI589397

VERSION AI589397.1 GI:4598445

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 34)

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013

DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 34

source

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2222853"

/clone\_lib="NCI-CGAP\_Panl"

```
/tissue_type="adenocarcinoma"  
/lab_host="DHL0B"  
/note="organ: pancreas; Vector: pcwv-SPORT6; site_1: SalI;  
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"
```

Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 83.33% Mismatches: 0  
 Query Match: 3.26% Indels: 0  
 DB: 17

US-09-375-514-22 (1-205) x A477888 (1-35)

QY 55 HisThrProHisProAla 60  
 Db 34 CACACCCCCACCCAGC 17  
 |||||||

RESULT 41

BH792266 36 bp DNA linear GSS 02-APR-2002  
 LOCUS SALK\_063236.51.15.x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_063236.51.15.x, DNA  
 sequence.

ACCESSION BH792266  
 VERSION BH792266.1 GI:19888854  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis;  
 1 (bases 1 to 36)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
 , Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome

JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated intron of At5g52330.  
 Class: TDNA tagged.

FEATURES  
 source Location/Qualifiers  
 1..36  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"

/clone="SALK\_063236.51.15.x"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT 13 a 4 c 8 g 11 t

Alignment Scores:  
 Pred. No.: 5.86e+05 Length: 36  
 Score: 36.00 Matches: 5  
 Percent Similarity: 87.50% Conservative: 2  
 Best Local Similarity: 62.50% Mismatches: 1  
 Query Match: 3.26% Indels: 0  
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x BH792266 (1-36)

QY 185 LeuHisThrTrpIleGlnAspAsn 192  
 Db 5 CTAGAGACATGTTGGAAGACAAT 28  
 |||

RESULT 42

AA987401/c  
 LOCUS

DEFINITION Oq87906.s1 NCI\_CGAP\_Kid6 Homo sapiens cdna clone IMAGE:1593370 3'  
 similar to TR:Q99322 Q99322 MOCIN CORE POLYPEPTIDE, TRACHEAL  
 ; contains element LI repetitive element ;, mRNA sequence.

ACCESSION AA987401  
 VERSION AA987401.1 GI:3172765  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 37)

REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.

FEATURES  
 source Location/Qualifiers

1..37  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1593370"  
 /clone\_lib="NCI\_CGAP\_Kid6"  
 /sex="mixed"  
 /tissue\_type="kidney tumor"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: kidney; Vector: Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'  
 GAATTCGCGACGAG 3' 3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

BASE COUNT 4 a 1 c 19 g 13 t

Alignment Scores:

Pred. No.: 6.04e+05 Length: 37  
 Score: 36.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 83.33% Mismatches: 0  
 Query Match: 3.26% Indels: 0  
 DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA987401 (1-37)

QY 55 HisThrProHisProAla 60  
 Db 30 CACACACACACCCATCA 13  
 |||||||

RESULT 43

AI357425 37 bp mRNA linear EST 15-FEB-1999  
 LOCUS qu01c09.x1 NCI\_CGAP\_Co14 Homo sapiens cdna clone IMAGE:1963504 3'  
 DEFINITION similar to SW:EXTN\_DAUCA P06599 EXTENSIN PRECURSOR. ; contains  
 MSRI.b3 MSRI repetitive element ;, mRNA sequence.

ACCESSION AI357425  
 VERSION AI357425.1 GI:4109046  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 37)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

Clone Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1215 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

## FEATURES

Location/Qualifiers

1..37

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1963504"

/clone\_lib="NCI-CGAP\_Col4"

/tissue\_type="moderately-differentiated adenocarcinoma"

/lab\_host="DH10B"

/note="Organ: Colon; Vector: PCMV-SPORT6; Site:1: SalI;

Site:2: NotI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.7 kb. Life Technologies catalog #:

11531-019"

5 a 25 c 7 g 0 t

## BASE COUNT

ORIGIN

## Alignment Scores:

Pred. No.: 5 6.04e+05 Length: 37

Score: 36.00 Matches: 7

Percent Similarity: 63.64% Conservative: 0

Best Local Similarity: 63.64% Mismatches: 4

Query Match: 3.26% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI357425 (1-37)

Qy 53 ProGlyH1sThrProH1sProAlaAlaSerArg 63

||||| ||||| ||||| ||||| |||||

5 CCGGAGCACCACCCCGCCCGCCGCGCACC 37

## RESULT 44

BI829358/c

## LOCUS

BI829358 603079491F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5170966 5',

linear EST 04-OCT-2001

mRNA sequence.

## DEFINITION

BI829358

## ACCESSION

BI829358

## VERSION

BI829358.1

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 38)

## AUTHORS

NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAML1425 row: f column: 23

High quality sequence stop: 38.

## FEATURES

Location/Qualifiers

1..38

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5170966"

/clone\_lib="NIH\_MGC\_119"

/tissue\_type="medulla"

/lab\_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORT6; Site:1: NotI;

Site:2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH\_MGC Library."

12 a 7 c 17 g 2 t

## BASE COUNT

ORIGIN

## Alignment Scores:

Pred. No.: 6.22e+05 Length: 38

Score: 36.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.26% Indels: 0

DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x BI829358 (1-38)

Qy 84 ProAlaLeuSerProValProPro 91

||||| ||||| ||||| ||||| |||||

36 CCGCTCTGTCCTCGCTGCTCCCA 13

## RESULT 45

AA869375/c

## LOCUS

AA869375

## DEFINITION

40 bp mRNA linear EST 16-MAR-1998

Vq07c10.r1 Barstead stromal cell line MPLR88 Mus musculus CDNA

clone IMAGE:1093554 5' similar to Tr:Q14883 Q14883 INTESINAL MUCIN

;; mRNA sequence.

## ACCESSION

AA869375

## VERSION

AA869375.1

## KEYWORDS

EST.

## SOURCE

house mouse.

## ORGANISM

Mus musculus

## REFERENCE

1 (bases 1 to 40)

## AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

## TITLE

The WashU-HMI Mouse EST Project

## JOURNAL

Unpublished (1996)

## COMMENT

Contact: Marra M/Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:599786

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES  
source

1. 40  
Location/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1093554"  
/clone\_lib="Barstead stromal cell line MPLRB8"  
/cell\_line="C2C12 (undifferentiated)"  
/lab\_host="DH10B"  
/note="Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCGCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Source undifferentiated tissue culture cell line C2C12. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins."

BASE COUNT 1 a 4 c 23 g 12 t

ORIGIN

Alignment Scores:

Pred. No.: 6.58e+05 Length: 40  
Score: 36.00 Matches: 5  
Percent Similarity: 85.71% Conservative: 1  
Best Local Similarity: 71.43% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AA869375 (1-40)

QY 53 ProGlyHisThrProHisPro 59

Db 40 CCCCACCACACCGGCCCA 20  
|||||:|||||

RESULT 46

AI565182/c

LOCUS

DEFINITION t56h10.x1 NCI\_CGAP\_Utl Homo sapiens cDNA clone IMAGE:2212867 3' similar to TR:Q01943 Q01943 EXTENSION ; contains element TAR1 repetitive element ; mRNA sequence.

ACCESSION

AI565182

VERSION

AI565182.1 GI:4523639

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 2429 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA-No.

Location/Qualifiers

source

1. 40

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2212867"  
/clone\_lib="NCI\_CGAP\_Utl"  
/tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

BASE COUNT 15 a 6 c 19 g 0 t

ORIGIN

Alignment Scores:

Pred. No.: 6.58e+05 Length: 40  
Score: 36.00 Matches: 7  
Percent Similarity: 66.67% Conservative: 1  
Best Local Similarity: 58.33% Mismatches: 4  
Query Match: 3.26% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x AI565182 (1-40)

QY 46 ProGlyIlePheSerSerGlnProGlyHisThrPro 57

Db 37 CCTTTTTCCTTCCTCCCGGGGGGTCCCCC 2  
|||||:|||||

RESULT 47

AZ372178/c

LOCUS

DEFINITION 1M0123J24R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0123J24 R, DNA sequence.

ACCESSION

AZ372178

VERSION

AZ372178.1 GI:10485878

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0123 row: J column: 24

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1. 40

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0123J24"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson



## Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 9 a 6 c 15 g 10 t  
ORIGIN

Alignment Scores: Length: 40  
Pred. No.: 6.58e+05 Matches: 7  
Score: 36.00  
Percent Similarity: 61.54% Conservative: 1  
Best Local Similarity: 53.85% Mismatches: 5  
Query Match: 3.26% Indels: 0  
DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AZ372178 (1-40)

QY 86 LeuSerProValProValHisLeuAlaLeuArg 98

Db 40 CTCAACCTGCTCCACAGCTCTCGAAATCTCTACTAGG 2

RESULT 48

BE867536/c

LOCUS BE867536 38 bp mRNA linear EST 20-OCT-2000

DEFINITION 601443035F1 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE:3847280 5', mRNA sequence.

ACCESSION BE867536

VERSION BE867536.1 GI:10316312

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9561 row: e column: 09

High quality sequence stop: 38.

FEATURES

Location/Qualifiers

1..38

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3847280"

/clone\_lib="NIH MGC\_65"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.8 kb. Library constructed by Life

Technologies."

BASE COUNT 4 a 16 c 16 g 2 t

ORIGIN

Alignment Scores:

Pred. No.: 6.83e+05 Length: 38

Score: 35.50 Matches: 8

Percent Similarity: 76.92% Conservative: 2

Best Local Similarity: 61.54% Mismatches: 2

Query Match: 3.22% Indels: 1

DB: 12 Gaps: 1

US-09-375-514-22 (1-205) x BE867536 (1-38)

QY 36 GlyAlaAlaProGlyAlaAlaProAlaProGlyIle 48

Db 36 GGCTCTCG---CGGGCCCGCGCGCCGCCGAGGTA 1

RESULT 49

AI024239

LOCUS

DEFINITION AI024239 25 bp mRNA linear EST 18-JUN-1998

3' similar to TR:002402 002402 INSOLUBLE PROTEIN. ;, mRNA sequence.

ACCESSION AI024239

VERSION AI024239.1 GI:3239283

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo

, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40ml3 fwd. EF from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1642802"

/clone\_lib="Soares\_testis\_NHT"

/sex="male"

/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 14 c 0 g 1 t

ORIGIN

Alignment Scores:

Pred. No.: 4.72e+05 Length: 25

Score: 35.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.17% Indels: 0  
DB: 9 Gaps: 0  
US-09-375-514-22 (1-205) x A1024239 (1-25)  
QY 55 HisThProHisPro 59  
DB 3 CACACACACACCCA 17

RESULT 50  
AZ791470/c  
LOCUS 2M0041H21F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
DEFINITION clone UUGC2M0041H21 F, DNA sequence.

ACCESSION AZ791470  
VERSION AZ791470.1 GI:12934389  
KEYWORDS GSS.  
SOURCE house mouse.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
1 (bases 1 to 30)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0041 row: H column: 21

Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1..30

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0041H21"

/clone\_lib="Mouse 10kb plasmid UUGCLM library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (g11473211419b1AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

5 a 1 c 17 g

BASE COUNT  
ORIGIN

Alignment Scores:  
Pred. No.: 5.78e+05  
Score: 35.00  
Percent Similarity: 75.00%  
Best Local Similarity: 75.00%  
Query Match: 3.17%  
DB: 17  
US-09-375-514-22 (1-205) x AZ791470 (1-30)

QY 84 ProAlaLeuSerProValProPro 91

DB 28 CCACCTCTCTCAGCCCACTCCACCC 5

Search completed: May 31, 2003, 23:22:20  
Job time : 1377 secs



GenCore version 5.1.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: May 31, 2003, 22:26:00 ; Search time 126 Seconds  
(without alignments)  
2193.769 Million cell updates/sec

Title: US-09-375-514-22

Perfect score: 1104  
Sequence: 1 MAHAGRTGVDNREIVMKYIH.....HTWIQDNGWVGASGDVSLG 205

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 471450

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool/US09375514/runat\_28052003\_165346\_18724/app\_query.fasta\_1.391  
-DB=published Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LISP=500 -DOCLIGN=200 -THR SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500  
-MINLEN=10 -MAXLEN=40  
-USER=US09375514.@cgn2\_1\_98@runat\_28052003\_165346\_18724 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAPP -LARGEQUERY -NRG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44	4.0	24	9	US-09-970-820-11
C 2	44	4.0	24	9	US-09-986-718-11
C 3	44	4.0	24	10	US-09-371-900-11
C 1	44	4.0	24	9	US-09-970-820-11
C 2	44	4.0	24	9	US-09-986-718-11
C 3	44	4.0	24	10	US-09-371-900-11

Sequence 18, Appl	33	3.8	42	C 4	9	US-09-963-761B-18	Sequence 18, Appl
Sequence 3, Appl1	31	3.7	41	C 5	10	US-09-925-67A-3	Sequence 3, Appl1
Sequence 465, App	31	3.5	39	C 6	10	US-09-801-274-465	Sequence 465, App
Sequence 372, App	31	3.5	38.5	C 7	10	US-09-801-274-465	Sequence 372, App
Sequence 21, Appl	22	3.4	38	C 8	9	US-09-931-732-21	Sequence 21, Appl
Sequence 2, Appl1	30	3.4	38	C 9	9	US-09-984-842-2	Sequence 2, Appl1
Sequence 943, App	31	3.4	38	C 10	10	US-09-801-274-943	Sequence 943, App
Sequence 370, App	38	3.4	38	C 11	9	US-10-125-635A-370	Sequence 370, App
Sequence 370, App	38	3.4	38	C 12	9	US-09-938-864-370	Sequence 370, App
Sequence 370, App	38	3.4	38	C 13	9	US-09-785-019-370	Sequence 370, App
Sequence 370, App	38	3.4	38	C 14	9	US-10-002-603-370	Sequence 370, App
Sequence 11, Appl	37	3.4	37	C 15	24	US-09-920-342-11	Sequence 11, Appl
Sequence 2701, Ap	25	3.4	37	C 16	9	US-10-060-756A-2701	Sequence 2701, Ap
Sequence 1740, Ap	31	3.4	37	C 17	10	US-09-801-274-1740	Sequence 1740, Ap
Sequence 34, Appl	33	3.4	37	C 18	9	US-09-874-503-34	Sequence 34, Appl
Sequence 34, Appl	33	3.4	37	C 19	9	US-10-000-157-34	Sequence 34, Appl
Sequence 34, Appl	33	3.4	37	C 20	9	US-09-747-259-34	Sequence 34, Appl
Sequence 34, Appl	33	3.4	37	C 21	9	US-09-908-827-34	Sequence 34, Appl
Sequence 71, Appl	33	3.4	37	C 22	40	US-09-245-802-71	Sequence 71, Appl
Sequence 34, Appl	20	3.3	36	C 23	10	US-09-734-846-34	Sequence 34, Appl
Sequence 45, Appl	20	3.3	36	C 24	10	US-09-734-847A-45	Sequence 45, Appl
Sequence 37, Appl	25	3.3	36	C 25	9	US-09-911-904-37	Sequence 37, Appl
Sequence 4774, Ap	25	3.3	36	C 26	10	US-09-866-108-4774	Sequence 4774, Ap
Sequence 4775, Ap	25	3.3	36	C 27	10	US-09-866-108-4775	Sequence 4775, Ap
Sequence 4776, Ap	25	3.3	36	C 28	10	US-09-866-108-4776	Sequence 4776, Ap
Sequence 4777, Ap	25	3.3	36	C 29	10	US-09-866-108-4777	Sequence 4777, Ap
Sequence 4778, Ap	25	3.3	36	C 30	10	US-09-866-108-4778	Sequence 4778, Ap
Sequence 4779, Ap	25	3.3	36	C 31	10	US-09-866-108-4779	Sequence 4779, Ap
Sequence 4780, Ap	25	3.3	36	C 32	10	US-09-866-108-4780	Sequence 4780, Ap
Sequence 4781, Ap	25	3.3	36	C 33	10	US-09-866-108-4781	Sequence 4781, Ap
Sequence 11, Appl	28	3.3	36	C 34	10	US-09-817-387-11	Sequence 11, Appl
Sequence 28, Appl	29	3.3	36	C 35	10	US-09-949-145-28	Sequence 28, Appl
Sequence 8, Appl1	30	3.3	36	C 36	10	US-10-245-206-8	Sequence 8, Appl1
Sequence 8, Appl1	30	3.3	36	C 37	10	US-09-291-129-8	Sequence 8, Appl1
Sequence 1215, Ap	31	3.3	36	C 38	10	US-09-801-274-1215	Sequence 1215, Ap
Sequence 15, Appl	32	3.3	36	C 39	10	US-09-854-356-15	Sequence 15, Appl
Sequence 23, Appl	32	3.3	36	C 40	10	US-10-000-512-23	Sequence 23, Appl
Sequence 31, Appl	35	3.3	36	C 41	10	US-09-473-872-31	Sequence 31, Appl
Sequence 78, Appl	39	3.3	36	C 42	10	US-09-894-633A-78	Sequence 78, Appl
Sequence 2, Appl1	39	3.3	36	C 43	10	US-09-735-363A-2	Sequence 2, Appl1
Sequence 67, Appl	27	3.2	35.5	C 44	10	US-09-735-363A-67	Sequence 67, Appl
Sequence 4465, Ap	27	3.2	35.5	C 45	10	US-09-866-108-4465	Sequence 4465, Ap
Sequence 4466, Ap	25	3.2	35	C 46	10	US-09-866-108-4466	Sequence 4466, Ap
Sequence 4467, Ap	25	3.2	35	C 47	10	US-09-866-108-4467	Sequence 4467, Ap
Sequence 4468, Ap	25	3.2	35	C 48	10	US-09-866-108-4468	Sequence 4468, Ap
Sequence 4469, Ap	25	3.2	35	C 49	10	US-09-866-108-4469	Sequence 4469, Ap
Sequence 4470, Ap	25	3.2	35	C 50	10	US-09-866-108-4470	Sequence 4470, Ap
Sequence 4471, Ap	25	3.2	35	C 51	10	US-09-866-108-4471	Sequence 4471, Ap
Sequence 4472, Ap	25	3.2	35	C 52	10	US-09-866-108-4472	Sequence 4472, Ap
Sequence 15, Appl	30	3.2	35	C 53	8	US-08-796-570A-15	Sequence 15, Appl
Sequence 15, Appl	30	3.2	35	C 54	9	US-10-067-477-15	Sequence 15, Appl
Sequence 18, Appl	30	3.2	35	C 55	10	US-09-924-439-18	Sequence 18, Appl
Sequence 16, Appl	32	3.2	35	C 56	10	US-10-114-482-16	Sequence 16, Appl
Sequence 19, Appl	30	3.2	35	C 57	12	US-10-114-482-19	Sequence 19, Appl
Sequence 722, App	31	3.2	35	C 58	10	US-09-801-274-722	Sequence 722, App
Sequence 1579, Ap	31	3.2	35	C 59	10	US-09-801-274-1579	Sequence 1579, Ap
Sequence 1, Appl1	33	3.2	35	C 60	10	US-09-925-674A-1	Sequence 1, Appl1
Sequence 5, Appl1	33	3.2	35	C 61	10	US-09-925-674A-5	Sequence 5, Appl1
Sequence 5, Appl1	35	3.2	35	C 62	37	US-09-913-238-5	Sequence 5, Appl1
Sequence 4006, Ap	37	3.2	35	C 63	9	US-09-877-478-4006	Sequence 4006, Ap
Sequence 49, Appl	37	3.2	35	C 64	9	US-09-500-700-49	Sequence 49, Appl
Sequence 24, Appl	38	3.2	35	C 65	9	US-09-832-648-24	Sequence 24, Appl
Sequence 1, Appl1	34	3.1	34	C 66	19	US-09-932-129-1	Sequence 1, Appl1
Sequence 64, Appl	19	3.1	34	C 67	19	US-09-734-847A-64	Sequence 64, Appl
Sequence 65, Appl	20	3.1	34	C 68	10	US-09-734-847A-65	Sequence 65, Appl
Sequence 7, Appl1	20	3.1	34	C 69	10	US-09-832-648-7	Sequence 7, Appl1
Sequence 23, Appl	20	3.1	34	C 70	10	US-09-832-648-23	Sequence 23, Appl
Sequence 936, App	20	3.1	34	C 71	20	US-09-827-998-936	Sequence 936, App
Sequence 937, App	25	3.1	34	C 72	10	US-09-827-998-937	Sequence 937, App
Sequence 116, App	25	3.1	34	C 73	10	US-08-591-486B-116	Sequence 116, App
Sequence 51, Appl	28	3.1	34	C 74	8	US-09-953-052-51	Sequence 51, Appl
Sequence 6, Appl1	30	3.1	34	C 75	9	US-10-175-268-6	Sequence 6, Appl1

77	34	3.1	30	10	US-09-803-552-6	Sequence 6, Appli	150	34	3.1	38	10	US-09-987-456-36	Sequence 36, Appli
78	34	3.1	30	10	US-09-803-347-6	Sequence 6, Appli	c 151	34	3.1	39	9	US-10-085-056-29	Sequence 29, Appli
79	34	3.1	30	10	US-09-803-549-6	Sequence 6, Appli	c 152	34	3.1	39	9	US-10-080-980-24	Sequence 24, Appli
80	34	3.1	30	10	US-09-803-402-6	Sequence 6, Appli	c 153	34	3.1	39	9	US-10-100-957A-147	Sequence 147, Appli
81	34	3.1	30	10	US-09-968-445-6	Sequence 6, Appli	c 154	34	3.1	39	10	US-09-987-456-66	Sequence 66, Appli
c 82	34	3.1	31	9	US-09-912-263-456	Sequence 456, App	155	33.5	3.0	35	9	US-09-991-470-7	Sequence 7, Appli
83	34	3.1	31	9	US-09-848-754A-7017	Sequence 7017, Ap	156	33.5	3.0	36	9	US-09-861-257-69	Sequence 69, Appli
c 84	34	3.1	31	10	US-09-801-274-1262	Sequence 1262, Ap	157	33	3.0	17	9	US-10-029-598-30	Sequence 30, Appli
c 85	34	3.1	31	10	US-09-801-274-1347	Sequence 1347, Ap	158	33	3.0	20	9	US-09-828-344-24	Sequence 24, Appli
c 86	34	3.1	32	9	US-10-282-602-5	Sequence 5, Appli	159	33	3.0	20	9	US-10-215-271-18	Sequence 18, Appli
87	34	3.1	36	9	US-09-966-781A-15	Sequence 15, Appli	160	33	3.0	20	9	US-10-215-271-30	Sequence 30, Appli
88	34	3.1	36	10	US-09-932-129-4	Sequence 4, Appli	c 161	33	3.0	21	9	US-09-959-519-7	Sequence 7, Appli
89	34	3.1	37	9	US-09-992-588-463	Sequence 463, App	c 162	33	3.0	24	9	US-09-991-936-1932	Sequence 1932, Ap
90	34	3.1	37	9	US-09-989-293A-463	Sequence 463, App	c 163	33	3.0	25	9	US-10-215-112-4514	Sequence 4514, Ap
91	34	3.1	37	9	US-09-989-735-463	Sequence 463, App	c 164	33	3.0	25	9	US-10-215-112-4515	Sequence 4515, Ap
92	34	3.1	37	9	US-09-990-444-463	Sequence 463, App	c 165	33	3.0	25	9	US-10-215-112-4638	Sequence 4638, Ap
93	34	3.1	37	9	US-09-989-730-463	Sequence 463, App	c 166	33	3.0	25	9	US-10-215-112-4639	Sequence 4639, Ap
94	34	3.1	37	9	US-09-990-436-463	Sequence 463, App	c 167	33	3.0	25	9	US-10-215-112-4784	Sequence 4784, Ap
95	34	3.1	37	9	US-09-991-181-463	Sequence 463, App	c 168	33	3.0	25	9	US-10-215-112-8311	Sequence 8311, Ap
96	34	3.1	37	9	US-09-993-687-463	Sequence 463, App	c 169	33	3.0	25	9	US-10-215-112-8437	Sequence 8437, Ap
97	34	3.1	37	9	US-09-989-734-463	Sequence 463, App	c 170	33	3.0	25	9	US-10-215-112-11553	Sequence 11553, A
98	34	3.1	37	9	US-09-997-653-463	Sequence 463, App	c 171	33	3.0	25	9	US-10-215-112-11554	Sequence 11554, A
99	34	3.1	37	9	US-09-993-667-463	Sequence 463, App	c 172	33	3.0	25	9	US-10-215-112-11555	Sequence 11555, A
100	34	3.1	37	9	US-09-990-438-463	Sequence 463, App	c 173	33	3.0	25	10	US-09-866-108-3926	Sequence 3926, Ap
101	34	3.1	37	9	US-09-990-562-463	Sequence 463, App	c 174	33	3.0	25	10	US-09-866-108-3927	Sequence 3927, Ap
102	34	3.1	37	9	US-09-997-428-463	Sequence 463, App	c 175	33	3.0	25	10	US-09-866-108-4413	Sequence 4413, Ap
103	34	3.1	37	9	US-09-997-666-463	Sequence 463, App	c 176	33	3.0	25	10	US-09-866-108-4414	Sequence 4414, Ap
104	34	3.1	37	9	US-09-990-711-463	Sequence 463, App	c 177	33	3.0	25	10	US-09-866-108-13254	Sequence 13254, A
105	34	3.1	37	9	US-09-989-726-463	Sequence 463, App	c 178	33	3.0	25	10	US-09-866-108-13255	Sequence 13255, A
106	34	3.1	37	9	US-09-990-437-463	Sequence 463, App	c 179	33	3.0	25	10	US-09-866-108-13256	Sequence 13256, A
107	34	3.1	37	9	US-09-998-156-463	Sequence 463, App	c 180	33	3.0	25	10	US-09-866-108-13257	Sequence 13257, A
108	34	3.1	37	9	US-09-991-157-463	Sequence 463, App	c 181	33	3.0	25	10	US-09-866-108-13258	Sequence 13258, A
109	34	3.1	37	9	US-09-991-172-463	Sequence 463, App	c 182	33	3.0	25	10	US-09-827-998-933	Sequence 933, App
110	34	3.1	37	9	US-09-997-514-463	Sequence 463, App	c 183	33	3.0	25	10	US-09-827-998-938	Sequence 938, App
111	34	3.1	37	9	US-09-997-573-463	Sequence 463, App	c 184	33	3.0	25	10	US-09-827-998-939	Sequence 939, App
112	34	3.1	37	9	US-09-990-443-463	Sequence 463, App	c 185	33	3.0	25	10	US-09-827-998-940	Sequence 940, App
113	34	3.1	37	9	US-09-990-726-463	Sequence 463, App	c 186	33	3.0	25	10	US-09-827-998-941	Sequence 941, App
114	34	3.1	37	9	US-09-997-559-463	Sequence 463, App	c 187	33	3.0	28	10	US-09-835-381-11	Sequence 11, Appli
115	34	3.1	37	9	US-09-991-172-463	Sequence 463, App	c 188	33	3.0	30	9	US-09-364-847-24	Sequence 24, Appli
c 116	34	3.1	37	9	US-09-780-533A-4334	Sequence 4334, Ap	c 189	33	3.0	30	9	US-09-364-847-40	Sequence 40, Appli
117	34	3.1	37	9	US-09-989-729A-463	Sequence 463, App	c 190	33	3.0	30	10	US-09-738-847-3	Sequence 3, Appli
118	34	3.1	37	9	US-09-990-440-463	Sequence 463, App	c 191	33	3.0	31	9	US-09-912-263-320	Sequence 320, App
119	34	3.1	37	9	US-09-991-854-463	Sequence 463, App	c 192	33	3.0	31	9	US-09-959-987-10	Sequence 10, Appli
120	34	3.1	37	9	US-09-997-349-463	Sequence 463, App	c 193	33	3.0	31	9	US-09-776-474-2455	Sequence 2455, Ap
121	34	3.1	37	9	US-09-997-440-463	Sequence 463, App	c 194	33	3.0	31	10	US-09-801-274-1486	Sequence 1486, Ap
122	34	3.1	37	9	US-09-997-628-463	Sequence 463, App	c 195	33	3.0	31	10	US-09-944-411-21	Sequence 21, Appli
123	34	3.1	37	9	US-09-997-683-463	Sequence 463, App	c 196	33	3.0	31	10	US-09-759-352-19	Sequence 19, Appli
124	34	3.1	37	9	US-09-993-469-463	Sequence 463, App	c 197	33	3.0	31	10	US-09-900-530A-42	Sequence 42, Appli
125	34	3.1	37	9	US-09-993-748-463	Sequence 463, App	c 198	33	3.0	32	9	US-10-221-841-4	Sequence 4, Appli
126	34	3.1	37	9	US-09-997-542-463	Sequence 463, App	c 199	33	3.0	32	9	US-10-116-420-30	Sequence 30, Appli
127	34	3.1	37	9	US-09-990-427-463	Sequence 463, App	c 200	33	3.0	33	9	US-09-863-733A-30	Sequence 30, Appli
128	34	3.1	37	9	US-09-990-439-463	Sequence 463, App	c 201	33	3.0	35	9	US-09-837-621-33	Sequence 33, Appli
129	34	3.1	37	9	US-09-989-328-463	Sequence 463, App	c 202	33	3.0	35	10	US-09-788-038-33	Sequence 33, Appli
130	34	3.1	37	9	US-09-993-583-463	Sequence 463, App	c 203	33	3.0	35	10	US-09-975-374A-3	Sequence 3, Appli
131	34	3.1	37	9	US-09-991-073-463	Sequence 463, App	c 204	33	3.0	35	10	US-09-504-231A-1779	Sequence 1779, Ap
132	34	3.1	37	9	US-09-941-992-463	Sequence 463, App	c 205	33	3.0	36	10	US-09-274-553B-1779	Sequence 50, Appli
133	34	3.1	37	9	US-09-992-521-463	Sequence 463, App	c 206	33	3.0	38	10	US-09-179-536B-136	Sequence 136, App
134	34	3.1	37	9	US-09-997-333-463	Sequence 463, App	c 207	33	3.0	38	10	US-09-765-272-337	Sequence 337, App
135	34	3.1	37	9	US-09-997-384-463	Sequence 463, App	c 208	33	3.0	38	10	US-09-987-456-34	Sequence 34, Appli
136	34	3.1	37	10	US-09-989-722-463	Sequence 463, App	c 209	33	3.0	39	10	US-09-931-180-34	Sequence 34, Appli
137	34	3.1	37	10	US-09-989-723-463	Sequence 463, App	c 210	33	3.0	39	10	US-09-987-456-61	Sequence 61, Appli
138	34	3.1	37	10	US-09-989-727-463	Sequence 463, App	c 211	33	3.0	39	10	US-09-892-613C-29	Sequence 29, Appli
139	34	3.1	37	10	US-09-853-033-14	Sequence 14, Appli	c 212	33	3.0	40	10	US-09-245-802-4	Sequence 4, Appli
140	34	3.1	37	10	US-09-989-731-463	Sequence 463, App	c 213	33	3.0	36	9	US-10-185-815-69	Sequence 69, Appli
141	34	3.1	37	10	US-09-991-073-463	Sequence 463, App	c 214	33	3.0	36	9	US-09-800-266A-51	Sequence 51, Appli
142	34	3.1	37	10	US-09-990-442-463	Sequence 463, App	c 215	32.5	2.9	18	9	US-09-895-007A-51	Sequence 51, Appli
143	34	3.1	37	10	US-09-991-163-463	Sequence 463, App	c 216	32	2.9	18	9	US-10-023-909A-51	Sequence 51, Appli
144	34	3.1	37	10	US-09-991-163-463	Sequence 463, App	c 217	32	2.9	18	9	US-09-835-371-21	Sequence 21, Appli
145	34	3.1	37	10	US-09-993-604-463	Sequence 463, App	c 218	32	2.9	18	9	US-09-920-313-51	Sequence 51, Appli
146	34	3.1	37	10	US-09-990-456-463	Sequence 463, App	c 219	32	2.9	18	9	US-09-835-370-21	Sequence 21, Appli
147	34	3.1	37	10	US-09-989-721-463	Sequence 463, App	c 220	32	2.9	18	9	US-09-888-326-755	Sequence 755, App
148	34	3.1	38	9	US-10-057-558-32	Sequence 32, Appli	c 221	32	2.9	18	9		
149	34	3.1	38	9	US-10-072-438-25	Sequence 25, Appli	c 222	32	2.9	18	9		

c 223	18	9	US-09-888-326-756	Sequence 756, App	c 296	31	10	US-09-801-274-893	Sequence 893, App
c 224	18	9	US-09-931-732-20	Sequence 20, App	c 297	31	10	US-09-939-754-1	Sequence 1, Appl
c 225	18	9	US-09-818-918-55	Sequence 55, Appl	c 298	31	10	US-09-939-832-1	Sequence 1, Appl
c 226	18	9	US-10-112-653-1	Sequence 1, Appl	c 299	31	10	US-09-939-832-1	Sequence 55, Appl
c 227	18	9	US-10-112-653-85	Sequence 85, Appl	c 300	31	10	US-09-827-822-1	Sequence 1, Appl
c 228	18	9	US-10-017-995-1	Sequence 1, Appl	c 301	31	10	US-09-990-080-7	Sequence 7, Appl
c 229	18	9	US-10-017-995-54	Sequence 54, Appl	c 302	31	10	US-09-843-250-47	Sequence 47, Appl
c 230	18	9	US-10-017-995-55	Sequence 55, Appl	c 303	31	10	US-09-837-969A-3	Sequence 3, Appl
c 231	18	9	US-10-017-995-91	Sequence 91, Appl	c 304	31	10	US-09-915-060-46	Sequence 46, Appl
c 232	18	9	US-09-776-479-1	Sequence 1, Appl	c 305	31	10	US-09-915-060-51	Sequence 51, Appl
c 233	18	9	US-09-776-479-54	Sequence 54, Appl	c 306	31	10	US-09-841-321A-3	Sequence 3, Appl
c 234	18	9	US-09-776-479-55	Sequence 55, Appl	c 307	31	10	US-09-978-758-20	Sequence 20, Appl
c 235	18	9	US-09-776-479-91	Sequence 91, Appl	c 308	31	10	US-09-952-060-22	Sequence 22, Appl
c 236	18	9	US-10-002-884A-6	Sequence 6, Appl	c 309	31	10	US-09-377-885A-33	Sequence 33, Appl
c 237	18	9	US-10-300-247-51	Sequence 51, Appl	c 310	31	10	US-09-991-470-7	Sequence 7, Appl
c 238	18	10	US-09-734-846-68	Sequence 68, Appl	c 311	31	10	US-10-083-168-32	Sequence 32, Appl
c 239	18	10	US-09-824-468-59	Sequence 59, Appl	c 312	31	10	US-09-868-851-20	Sequence 20, Appl
c 240	18	10	US-09-824-468-104	Sequence 104, Appl	c 313	31	10	US-09-861-257-69	Sequence 69, Appl
c 241	18	10	US-09-969-373-4373	Sequence 4373, App	c 314	31	10	US-09-848-616-47	Sequence 47, Appl
c 242	18	10	US-09-965-116A-7	Sequence 7, Appl	c 315	31	10	US-10-240-072-4	Sequence 4, Appl
c 243	18	10	US-09-965-116A-77	Sequence 77, Appl	c 316	31	10	US-09-813-380-3	Sequence 3, Appl
c 244	18	10	US-09-965-116A-98	Sequence 98, Appl	c 317	31	10	US-09-813-380-4	Sequence 4, Appl
c 245	18	10	US-09-965-116A-99	Sequence 99, Appl	c 318	31	10	US-09-245-487B-25	Sequence 25, Appl
c 246	20	9	US-09-888-326-757	Sequence 12, Appl	c 319	31	10	US-09-245-487B-27	Sequence 27, Appl
c 247	20	9	US-09-888-326-766	Sequence 766, App	c 320	31	10	US-09-747-377-235	Sequence 235, App
c 248	20	9	US-09-932-300-72	Sequence 72, Appl	c 321	31	10	US-10-194-594-9	Sequence 9, Appl
c 249	20	9	US-10-112-653-81	Sequence 81, Appl	c 322	31	10	US-09-504-231A-3128	Sequence 3128, Ap
c 250	20	9	US-10-112-653-102	Sequence 102, App	c 323	31	10	US-09-774-553B-3128	Sequence 3128, Ap
c 251	20	9	US-10-017-995-87	Sequence 87, Appl	c 324	31	10	US-09-918-696-25	Sequence 25, Appl
c 252	20	9	US-10-017-995-109	Sequence 109, App	c 325	31	10	US-09-918-696-26	Sequence 26, Appl
c 253	20	9	US-09-776-479-87	Sequence 87, Appl	c 326	31	10	US-09-888-326-417	Sequence 417, App
c 254	20	9	US-09-776-479-109	Sequence 109, App	c 327	31	10	US-10-112-653-141	Sequence 141, App
c 255	20	9	US-10-074-246-14	Sequence 14, Appl	c 328	31	10	US-10-017-995-148	Sequence 148, App
c 256	21	9	US-09-765-081-398	Sequence 398, App	c 329	31	10	US-09-780-533A-3359	Sequence 3359, Ap
c 257	21	10	US-09-817-014-61	Sequence 61, Appl	c 330	31	10	US-09-776-479-148	Sequence 148, App
c 258	21	10	US-09-817-014-61	Sequence 61, Appl	c 331	31	10	US-09-308-207-47	Sequence 47, App
c 259	21	10	US-09-940-185-3361	Sequence 3361, App	c 332	31	10	US-09-756-186-12	Sequence 12, Appl
c 260	25	9	US-09-745-317-41	Sequence 41, Appl	c 333	31	10	US-09-473-872-33	Sequence 33, Appl
c 261	25	9	US-10-215-112-11552	Sequence 11552, A	c 334	31	10	US-09-946-175-35	Sequence 35, Appl
c 262	25	10	US-09-866-108-4386	Sequence 4386, Ap	c 335	31	10	US-09-966-277-29	Sequence 29, Appl
c 263	25	10	US-09-866-108-4387	Sequence 4387, Ap	c 336	31	10	US-09-918-696-13	Sequence 13, Appl
c 264	25	10	US-09-866-108-5162	Sequence 5162, Ap	c 337	31	10	US-09-918-696-14	Sequence 14, Appl
c 265	25	10	US-09-866-108-5163	Sequence 5163, Ap	c 338	31	10	US-09-966-930-29	Sequence 29, Appl
c 266	25	10	US-09-398-399-11	Sequence 11, Appl	c 339	31	10	US-09-245-802-94	Sequence 94, Appl
c 267	25	10	US-09-899-381-11	Sequence 11, Appl	c 340	31	10	US-09-974-974-13	Sequence 13, Appl
c 268	26	9	US-10-006-856A-92	Sequence 92, Appl	c 341	31	10	US-09-974-974-13	Sequence 13, Appl
c 269	26	9	US-10-006-818A-92	Sequence 92, Appl	c 342	31	10	US-10-181-846-121	Sequence 121, App
c 270	26	9	US-09-946-374-92	Sequence 92, Appl	c 343	31	10	US-09-734-846-29	Sequence 29, Appl
c 271	26	9	US-10-012-121A-92	Sequence 92, Appl	c 344	31	10	US-09-938-689-53	Sequence 53, Appl
c 272	26	9	US-10-012-121A-92	Sequence 92, Appl	c 345	31	10	US-10-006-856A-90	Sequence 90, Appl
c 273	26	9	US-10-015-869A-92	Sequence 92, Appl	c 346	31	10	US-10-006-818A-90	Sequence 90, Appl
c 274	26	9	US-10-006-116A-92	Sequence 92, Appl	c 347	31	10	US-10-015-393A-90	Sequence 90, Appl
c 275	26	9	US-10-006-117A-92	Sequence 92, Appl	c 348	31	10	US-09-946-374-90	Sequence 90, Appl
c 276	26	9	US-10-013-313A-92	Sequence 92, Appl	c 349	31	10	US-10-012-121A-90	Sequence 90, Appl
c 277	26	9	US-10-017-527A-92	Sequence 92, Appl	c 350	31	10	US-10-015-869A-90	Sequence 90, Appl
c 278	26	9	US-10-007-194A-92	Sequence 92, Appl	c 351	31	10	US-10-006-116A-90	Sequence 90, Appl
c 279	26	9	US-10-013-430A-92	Sequence 92, Appl	c 352	31	10	US-10-013-913A-90	Sequence 90, Appl
c 280	26	9	US-10-011-671A-92	Sequence 92, Appl	c 353	31	10	US-10-017-527A-90	Sequence 90, Appl
c 281	26	9	US-10-012-755A-92	Sequence 92, Appl	c 354	31	10	US-10-007-194A-90	Sequence 90, Appl
c 282	26	9	US-09-345-373-92	Sequence 92, Appl	c 355	31	10	US-10-013-430A-90	Sequence 90, Appl
c 283	28	9	US-09-345-373-114	Sequence 114, App	c 356	31	10	US-10-011-671A-90	Sequence 90, Appl
c 284	28	10	US-09-853-666-13	Sequence 13, Appl	c 357	31	10	US-10-012-755A-90	Sequence 90, Appl
c 285	28	10	US-09-991-936-51	Sequence 51, Appl	c 358	31	10	US-10-012-755A-90	Sequence 90, Appl
c 286	32	2	US-09-817-387-12	Sequence 12, Appl	c 359	31	10	US-09-940-244-195	Sequence 195, App
c 287	32	2	US-09-953-052-50	Sequence 50, Appl	c 360	31	10	US-09-949-427-95	Sequence 95, Appl
c 288	32	2	US-10-196-793A-40	Sequence 40, Appl	c 361	31	10	US-10-010-802-397	Sequence 397, App
c 289	32	2	US-09-804-682-80	Sequence 80, Appl	c 362	31	10	US-10-300-616-14	Sequence 14, Appl
c 290	32	2	US-10-158-895-29	Sequence 29, Appl	c 363	31	10	US-10-132-382-17	Sequence 17, Appl
c 291	32	2	US-09-939-833-1	Sequence 1, Appl	c 364	31	10	US-09-940-185-565	Sequence 565, App
c 292	32	2	US-09-912-263-108	Sequence 108, App	c 365	31	10	US-10-060-756A-2694	Sequence 2694, Ap
c 293	32	2	US-09-235-674-55	Sequence 55, Appl	c 366	31	10	US-10-060-756A-2695	Sequence 2695, Ap
c 294	32	2	US-09-801-274-112	Sequence 112, App	c 367	31	10	US-10-060-756A-2696	Sequence 2696, Ap
c 295	32	2	US-09-801-274-431	Sequence 431, App	c 368	31	10		

369	31	2.8	9	US-10-060-756A-2697-	Sequence 2697, Ap	c 442	31	2.8	33	10	US-09-962-993-5	Sequence 5, Appl
370	31	2.8	25	US-10-060-756A-2698	Sequence 2698, Ap	443	31	2.8	33	12	US-10-052-545-3	Sequence 3, Appl
371	31	2.8	25	US-10-060-756A-2699	Sequence 2699, Ap	444	31	2.8	34	9	US-10-060-841-37	Sequence 37, Appl
372	31	2.8	25	US-10-215-112-855	Sequence 855, App	445	31	2.8	34	9	US-10-093-958-30	Sequence 30, Appl
373	31	2.8	25	US-10-215-112-863	Sequence 863, App	446	31	2.8	34	9	US-10-093-958-32	Sequence 32, Appl
374	31	2.8	25	US-10-215-112-3003	Sequence 3003, Ap	447	31	2.8	34	9	US-09-848-616-46	Sequence 46, Appl
375	31	2.8	25	US-10-215-112-3509	Sequence 3509, Ap	448	31	2.8	35	9	US-09-773-593-10	Sequence 10, Appl
376	31	2.8	25	US-10-215-112-3635	Sequence 3635, Ap	449	31	2.8	35	9	US-09-733-042-40	Sequence 40, Appl
377	31	2.8	25	US-10-215-112-9820	Sequence 9820, Ap	450	31	2.8	35	9	US-09-376-940-21	Sequence 21, Appl
378	31	2.8	25	US-10-215-112-9932	Sequence 9932, Ap	451	31	2.8	35	9	US-10-066-127-21	Sequence 21, Appl
379	31	2.8	25	US-09-940-185-4333	Sequence 4333, Ap	452	31	2.8	35	10	US-09-732-618-39	Sequence 39, Appl
380	31	2.8	25	US-09-770-720-2	Sequence 2, Appl	453	31	2.8	35	10	US-09-765-272-302	Sequence 302, App
381	31	2.8	25	US-09-866-108-3928	Sequence 3928, Ap	454	31	2.8	36	9	US-10-149-121-20	Sequence 20, Appl
382	31	2.8	25	US-09-866-108-3929	Sequence 3929, Ap	455	31	2.8	36	10	US-09-804-733A-17	Sequence 17, Appl
383	31	2.8	25	US-09-866-108-3930	Sequence 3930, Ap	456	31	2.8	36	10	US-09-804-733A-18	Sequence 18, Appl
384	31	2.8	25	US-09-866-108-4388	Sequence 4388, Ap	457	31	2.8	36	10	US-09-815-837-104	Sequence 104, App
385	31	2.8	25	US-09-866-108-4389	Sequence 4389, Ap	458	31	2.8	36	10	US-09-944-411-15	Sequence 15, Appl
386	31	2.8	25	US-09-866-108-4390	Sequence 4390, Ap	459	31	2.8	36	10	US-09-759-352-9	Sequence 9, Appl
387	31	2.8	25	US-09-866-108-5606	Sequence 5606, Ap	460	31	2.8	37	9	US-09-309-196-71	Sequence 71, Appl
388	31	2.8	25	US-09-866-108-5607	Sequence 5607, Ap	461	31	2.8	37	9	US-09-953-354-87	Sequence 87, Appl
389	31	2.8	25	US-09-866-108-5608	Sequence 5608, Ap	462	31	2.8	37	9	US-10-125-648-18	Sequence 18, Appl
390	31	2.8	25	US-09-866-108-5609	Sequence 5609, Ap	463	31	2.8	37	9	US-09-776-474-1322	Sequence 1922, Ap
391	31	2.8	25	US-09-866-108-5610	Sequence 5610, Ap	464	31	2.8	37	9	US-09-776-474-1332	Sequence 1932, Ap
392	31	2.8	25	US-09-866-108-11101	Sequence 11101, A	465	31	2.8	37	9	US-09-930-423-2775	Sequence 2775, Ap
393	31	2.8	25	US-09-866-108-11102	Sequence 11102, A	466	31	2.8	37	9	US-09-930-423-2778	Sequence 2789, Ap
394	31	2.8	25	US-09-866-108-13837	Sequence 13837, A	467	31	2.8	38	9	US-09-900-379-20	Sequence 20, Appl
395	31	2.8	25	US-09-866-108-13838	Sequence 13838, A	468	31	2.8	38	9	US-09-500-700-51	Sequence 51, Appl
396	31	2.8	25	US-09-866-108-13839	Sequence 13839, A	469	31	2.8	38	9	US-09-780-533A-2845	Sequence 2845, Ap
397	31	2.8	25	US-09-866-108-13840	Sequence 13840, A	470	31	2.8	38	9	US-09-848-754A-5023	Sequence 5023, Ap
398	31	2.8	25	US-09-866-108-13841	Sequence 13841, A	471	31	2.8	38	10	US-09-769-864-20	Sequence 20, Appl
399	31	2.8	25	US-09-866-108-13917	Sequence 13917, A	472	31	2.8	38	10	US-09-848-164-20	Sequence 20, Appl
400	31	2.8	25	US-09-866-108-13918	Sequence 13918, A	473	31	2.8	38	10	US-09-874-547-31	Sequence 31, Appl
401	31	2.8	25	US-09-827-998-927	Sequence 927, App	474	31	2.8	39	9	US-09-765-272-382	Sequence 382, App
402	31	2.8	25	US-09-827-998-927	Sequence 927, App	475	31	2.8	39	9	US-10-087-993-19	Sequence 19, Appl
403	31	2.8	25	US-09-827-998-928	Sequence 928, App	476	31	2.8	39	9	US-09-918-696-17	Sequence 17, Appl
404	31	2.8	25	US-09-827-998-928	Sequence 928, App	477	31	2.8	39	9	US-09-918-696-18	Sequence 18, Appl
405	31	2.8	25	US-09-827-998-929	Sequence 929, App	478	31	2.8	39	9	US-10-081-347-13	Sequence 13, Appl
406	31	2.8	25	US-09-827-998-930	Sequence 930, App	479	31	2.8	39	9	US-10-067-790-47	Sequence 47, Appl
407	31	2.8	25	US-09-827-998-931	Sequence 931, App	480	31	2.8	39	9	US-10-067-892-47	Sequence 47, Appl
408	31	2.8	25	US-09-827-998-932	Sequence 932, App	481	31	2.8	39	9	US-09-539-382-47	Sequence 47, Appl
409	31	2.8	25	US-09-827-998-932	Sequence 932, App	482	31	2.8	39	9	US-10-067-893-47	Sequence 47, Appl
410	31	2.8	26	US-09-918-702-17	Sequence 17, Appl	483	31	2.8	39	9	US-10-100-679-8	Sequence 8, Appl
411	31	2.8	26	US-10-085-476-3	Sequence 3, Appl	484	31	2.8	39	9	US-10-004-633-26	Sequence 26, Appl
412	31	2.8	26	US-10-201-964-5	Sequence 5, Appl	485	31	2.8	39	10	US/09/242	Sequence 21, Appl
413	31	2.8	28	US-09-902-460-17	Sequence 17, Appl	486	31	2.8	39	10	US-09-473-872-30	Sequence 30, Appl
414	31	2.8	28	US-10-231-426-4	Sequence 4, Appl	487	31	2.8	39	10	US-09-473-872-30	Sequence 30, Appl
415	31	2.8	29	US-09-739-451-14	Sequence 14, Appl	488	31	2.8	39	10	US-09-473-872-32	Sequence 32, Appl
416	31	2.8	30	US-09-983-657-1	Sequence 1, Appl	489	31	2.8	39	10	US-09-946-175-30	Sequence 30, Appl
417	31	2.8	30	US-10-027-199-8	Sequence 8, Appl	490	31	2.8	39	10	US-09-905-999-11	Sequence 11, Appl
418	31	2.8	30	US-09-877-336-8	Sequence 8, Appl	491	31	2.8	39	10	US-09-902-741-3	Sequence 3, Appl
419	31	2.8	30	US-09-952-060-24	Sequence 24, Appl	492	31	2.8	40	9	US-10-101-392-14	Sequence 14, Appl
420	31	2.8	30	US-10-085-906-11	Sequence 11, Appl	493	31	2.8	40	9	US-09-988-626-141	Sequence 141, App
421	31	2.8	30	US-10-170-997-8	Sequence 8, Appl	494	31	2.8	40	9	US-10-112-488-61	Sequence 61, Appl
422	31	2.8	30	US-09-952-677-3	Sequence 3, Appl	495	31	2.8	40	10	US-09-753-436-30	Sequence 30, Appl
423	31	2.8	31	US-10-060-841-32	Sequence 32, Appl	496	31	2.8	31	9	US-10-072-036-29	Sequence 29, Appl
424	31	2.8	31	US-09-780-533A-5449	Sequence 5449, Ap	497	30.5	2.8	31	10	US-09-801-274-879	Sequence 879, App
425	31	2.8	31	US-09-766-396-13	Sequence 13, Appl	498	30.5	2.8	31	10	US-09-854-799-8	Sequence 8, Appl
426	31	2.8	31	US-09-801-274-634	Sequence 634, App	499	30.5	2.8	39	9	US-10-096-373-5	Sequence 5, Appl
427	31	2.8	31	US-09-801-274-680	Sequence 680, App	500	30.5	2.8				
428	31	2.8	31	US-09-801-274-1046	Sequence 1046, Ap							
429	31	2.8	31	US-09-801-274-1346	Sequence 1346, Ap							
430	31	2.8	32	US-10-062-375-13	Sequence 13, Appl							
431	31	2.8	32	US-09-854-356-17	Sequence 17, Appl							
432	31	2.8	32	US-10-010-920-54	Sequence 54, Appl							
433	31	2.8	32	US-09-957-483-60	Sequence 60, Appl							
434	31	2.8	32	US-10-008-721-54	Sequence 721-54							
435	31	2.8	32	US-10-112-488-56	Sequence 56, Appl							
436	31	2.8	32	US-09-814-786-35	Sequence 35, Appl							
437	31	2.8	33	US-09-991-496-89	Sequence 89, Appl							
438	31	2.8	33	US-10-027-961A-15	Sequence 15, Appl							
439	31	2.8	33	US-10-022-832-57	Sequence 57, Appl							
440	31	2.8	33	US-10-196-730-9	Sequence 9, Appl							
441	31	2.8	33	US-10-252-408-11	Sequence 11, Appl							
			33	US-09-874-923-89	Sequence 89, Appl							

RESULT 1  
US-09-970-820-11/c  
; Sequence 11, Application US/09970820  
; Patent No. US20020170077A1  
; GENERAL INFORMATION:  
; APPLICANT: FALSB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:



ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/970,820  
FILING DATE: 05-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-970-820-11

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-970-820-11 (1-24)

140 AspGlyValAsnTrpGlyArg 146  
|||||  
Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 2  
US-09-986-718-11/c  
Sequence 11, Application US/09986718  
Patent No. US20020178458A1  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,718  
FILING DATE: 09-No. US20020178458A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/485,573  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-986-718-11

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-986-718-11 (1-24)

140 AspGlyValAsnTrpGlyArg 146  
|||||  
Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 3  
US-09-371-900-11/c  
Sequence 11, Application US/09371900  
Patent No. US20020137700A1  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/371,900  
FILING DATE: 11-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A

Db 28 AACGAGCATTTCACATCCTTGGATCGC 2

RESULT 5  
US-09-925-674A-3/C  
; Sequence 3, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; TITLE OF INVENTION:

; SOFTWARE: PatentIn Ver. 2.1

OTHER INFORMATION: n is inosine

NAME/KEY: MODIFIEDBASE  
; LOCATION: 17

NAME/KEY: modified\_base

```

; LOCATION: 20
; OTHER INFORMATION: n is inosine

```

US-09-923-014A-3

Alignment Scores:  
prod No : 3 5e+03

score:	41.00
percent	75.00%

Best Local Similarity: 75.00%

DB: 10

US-09-375-514-22 (1-205) x US-09-92

QY 188 TrpIleGlnAspAsnGlyGlyTrp

Db 31 TGGATCCAAGANMANGNGGCTGG

## RESULT 6

US-09-801-274-465  
 . Sequence 465 Application PS/0980

; Patent No. US20020032319A1

; APPLICANT: Cargill, Michele

APPLICANT: Lander, Eric S.

FILE REFERENCE: 2825.2009-001

; CURRENT AFFILIATION NUMBER: 05/0  
 : CURRENT FILING DATE: 2001-03-07

;; PRIOR APPLICATION NUMBER: US 60/  
: PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 607  
 ; PRIOR FILING DATE: 2000-05-22

; NUMBER OF SEQ ID NOS: 1802

; SEQ ID NO 465

TYPE: DNA

US-09-801-274-465

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-21

Alignment Scores:
Pred. No.: 4,74e+03      Length: 22
Score: 38.00             Matches: 7
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 3.44%              Indels: 0
DB: 9                       Gaps: 0

US-09-375-514-22 (1-205) x US-09-931-732-21 (1-22)

QY 89 valProProValValHisLeu 95
|||||
DB 2 GTGCCACCTGTGTCCACCTG 22

RESULT 9
US-09-984-842-2/c
; Sequence 2, Application US/0984842
; Publication No. US2003007752A1
; GENERAL INFORMATION:
; APPLICANT: MORTEN, JOHN EDWARD NORRIS
; TITLE OF INVENTION: METHODS FOR ANALYZING LTC4 SYNTHASE POLYMO
; TITLE OF INVENTION: DIAGNOSTIC USE
; FILE REFERENCE: PLS/009901/0282943
; CURRENT APPLICATION NUMBER: US/09/984,842
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/485,636
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: GB 9717766.1
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02468
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-984-842-2

Alignment Scores:
Pred. No.: 6.83e+03      Length: 30
Score: 38.00             Matches: 7
Percent Similarity: 87.50%      Conservative: 0
Best Local Similarity: 87.50%    Mismatches: 1
Query Match: 3.44%              Indels: 0
DB: 9                       Gaps: 0

US-09-375-514-22 (1-205) x US-09-984-842-2 (1-30)

QY 38 AlaProProGlyAlaAlaProAla 45
|||||
DB 29 GCCCGCGCTGGAGCGCCCGCCGCC 6

RESULT 10
US-09-801-274-943/c
; Sequence 943, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510

```

```
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-943

Alignment Scores:
Pred. No.: 7.09e+03      Length: 31
Score: 38.00             Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.44%      Indels: 0
DB: 10                   Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-943 (1-31)
QY 40 ProGlyAlaProGly 47
Db 31 CCAGGTCGCTCCACCCCTGGG 8

RESULT 11
US-10-125-635A-370/c
; Sequence 370, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-125-635A-370

Alignment Scores:
Pred. No.: 9.01e+03      Length: 38
Score: 38.00             Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44%      Indels: 0
DB: 9                     Gaps: 0

US-09-375-514-22 (1-205) x US-10-125-635A-370 (1-38)
QY 36 GlyAlaAlaProGlyAlaAlaPro 46
Db 35 GGTCCAGCAGCTCCGCCGCAACGCCCCACCG 3

RESULT 12
US-09-938-864-370/c
; Sequence 370, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly

; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Paul R.
; APPLICANT: Sleath, Thomas S.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-938-864-370

Alignment Scores:
Pred. No.: 9.01e+03      Length: 38
Score: 38.00             Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44%      Indels: 0
DB: 9                     Gaps: 0

US-09-375-514-22 (1-205) x US-09-785-019-370 (1-38)
QY 36 GlyAlaAlaProGlyAlaAlaPro 46
Db 35 GGTCCAGCAGCTCCGCCGCAACGCCCCACCG 3

RESULT 13
US-09-785-019-370/c
; Sequence 370, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Paul
; APPLICANT: Sleath, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-785-019-370

Alignment Scores:
Pred. No.: 9.01e+03      Length: 38
Score: 38.00             Matches: 7
Percent Similarity: 63.64% Conservative: 0
Best Local Similarity: 63.64% Mismatches: 4
Query Match: 3.44%      Indels: 0
DB: 9                     Gaps: 0

US-09-375-514-22 (1-205) x US-09-785-019-370 (1-38)
```

QY 36 GlyAlaAlaProProGlyAlaAlaProAlaPro 46  
||| ||||| ||| ||| |||  
Db 35 GGTCCAGCACCTCCGCCCGCCAGCCGCCACCG 3

## RESULT 14

US-10-002-603-370/c  
; Sequence 370, Application US/10002603  
; Publication No. US20030095971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Mossman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C6  
; CURRENT APPLICATION NUMBER: US/10/002,603  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 370  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-002-603-370

Alignment Scores:  
Pred. No.: 9,01e+03 Length: 38  
Score: 38.00 Matches: 7  
Percent Similarity: 63.64% Conservative: 0  
Best Local Similarity: 63.64% Mismatches: 4  
Query Match: 3.44% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-002-603-370 (1-38)

QY 36 GlyAlaAlaProProGlyAlaAlaProAlaPro 46  
||| ||||| ||| ||| |||  
Db 35 GGTCCAGCACCTCCGCCCGCCAGCCGCCACCG 3

## RESULT 15

US-09-920-342-11  
; Sequence 11, Application US/09920342  
; Patent No. US20020137709A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Southern California  
; APPLICANT: Lin, Shi-lung  
; APPLICANT: Chuong, Cheng-Ming  
; APPLICANT: Widelitz, Randall B.  
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS  
; FILE REFERENCE: 13761-7024  
; CURRENT APPLICATION NUMBER: US/09/920,342  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 60/222,479  
; PRIOR FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: bcl2 primer  
US-09-920-342-11

Alignment Scores:  
Pred. No.: 6,64e+03 Length: 24  
Score: 37.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.35% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-920-342-11 (1-24)

QY 177 MetThrGluTyrLeuAsnArg 183  
||||| ||||| ||||| |||||  
Db 3 ATGACTGAGTACCTGAACCG 23

## RESULT 16

US-10-060-756A-2700  
; Sequence 2700, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2700  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-2700

Alignment Scores:  
Pred. No.: 6,97e+03 Length: 25  
Score: 37.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 3.35% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-060-756A-2700 (1-25)

QY 39 ProProGlyAlaAlaProAlaPro 46  
||||| ||||| ||||| |||||  
Db 2 CCTCCAGAGGAGCACCAGCCCA 25

## RESULT 17

US-10-060-756A-2701  
; Sequence 2701, Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 2701  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-756A-2701

Alignment Scores:  
Pred. No.: 6.97e+03 Length: 25  
Score: 37.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 3.35% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-060-756A-2701 (1-25)

Qy 39 PROTGlyAlaAlaProAlaPro 46

Db 1 CCTCCAGGAGGACCCGGAAGCCA 24

RESULT 18

US-09-801-274-1740/c  
; Sequence 1740, Application US/09801274  
; Patent No. US20020032319A1  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2009-001  
; CURRENT APPLICATION NUMBER: US/09/801,274  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/187,510  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 60/206,129  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 1802  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1740  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-274-1740

Alignment Scores:  
Pred. No.: 8.98e+03 Length: 31  
Score: 37.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 3.35% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-1740 (1-31)

Qy 190 GlnAspAsnGlyGlyTyrValGly 197

|||||:|||||

Db 30 CAGGACAGTGGCGRTGGTAGGC 7  
RESULT 19  
US-09-874-503-34/c  
; Sequence 34, Application US/09874503  
; Patent No. US20020177188A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah G.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasinik, Melissa A.  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: P1381R1C1P3(US)  
; CURRENT APPLICATION NUMBER: US/09/874,503  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/253,646  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/244,072  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/242,837  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/175,481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/191,007  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/213,807  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US 60/172,096  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/138,387  
; PRIOR FILING DATE: 1999-06-09  
; PRIOR APPLICATION NUMBER: US 60/134,287  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/131,022  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: US 60/130,232  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/854,208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US 09/854,280  
; PRIOR FILING DATE: 2001-05-20  
; PRIOR APPLICATION NUMBER: US 09/816,744  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 09/747,259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/644,848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: US 09/380,142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/380,138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: US PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US99/05028  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 34  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-874-503-34

Alignment Scores: 33  
Pred. No.: 9.66e+03  
Score: 37.00  
Matches: 6  
Percent Similarity: 87.50%  
Conservative: 1  
Best Local Similarity: 75.00%  
Mismatch: 1  
Query Match: 3.35%  
Indels: 0  
DB: 0  
Gaps: 0

US-09-375-514-22 (1-205) x US-09-874-503-34 (1-33)

OY 56 ThrProHisProAlaAlaSerArg 63

Db 25 ACACCCCATCTGTAGCCACCTCGC 2

RESULT 20

Sequence 34, Application US/10000157  
Publication No. US20020182673A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul L.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hymowitz, Sarah  
APPLICANT: Tumas, Daniel  
APPLICANT: Starovasnik, Melissa.  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1CIP4 (US)  
CURRENT APPLICATION NUMBER: US/10/000,157

CURRENT FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/253646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/908827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10

```
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 34
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-10-000-157-34
Alignment Scores:
Pred. No.: 9.66e+03 Length: 33
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0
US-09-375-514-22 (1-205) x US-10-000-157-34 (1-33)
QY 56 ThrProHisProAlaAlaSerArg 63
Db 25 ACACCCCATCTGTAGCCACTGCG 2
RESULT 21
US-09-747-259-34/c
; Sequence 34, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tamas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
```

```
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 34
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-747-259-34
Alignment Scores:
Pred. No.: 9.66e+03 Length: 33
Score: 37.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 3.35% Indels: 0
DB: 9 Gaps: 0
US-09-375-514-22 (1-205) x US-09-747-259-34 (1-33)
QY 56 ThrProHisProAlaAlaSerArg 63
Db 25 ACACCCCATCTGTAGCCACTGCG 2
RESULT 22
US-09-908-827-34/c
; Sequence 34, Application US/09908827
; Publication No. US2003005442A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tamas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/908,827
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113,621
```



PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 34  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-908-827-34  
Alignment Scores:  
Pred. No.: 1,21e+04  
Score: 37.00  
Percent Similarity: 70.00%  
Best Local Similarity: 70.00%  
Query Match: 3.35%  
DB: 10  
US-09-375-514-22 (1-205) x US-09-245-802-71 (1-40)  
QY 51 SerGlnProGlyHisThrProHisProAla 60  
||||||| ||| ||| |||||

Pred. No.: 9.66e+03  
Score: 37.00  
Percent Similarity: 87.50%  
Best Local Similarity: 75.00%  
Query Match: 3.35%  
DB: 9  
US-09-375-514-22 (1-205) x US-09-908-827-34 (1-33)  
QY 56 ThrProHisProAlaSerArg 63  
||||||| |||:||||  
Db 25 ACACCCATCCTGTAGCCACTCGC 2  
RESULT 23  
US-09-245-802-71/c  
Sequence 71, Application US/09245802  
Patent No. US20010049125A1  
GENERAL INFORMATION:  
APPLICANT: STEMMER PH.D., WILLEM P.C.  
APPLICANT: LIPSHUTZ, ROBERT J.  
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION  
NUMBER OF SEQUENCES: 136  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/245,802  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/675,502  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/05480  
FILING DATE: 18-APR-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY, ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 16528J-015410US  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
US-09-245-802-71  
Alignment Scores:  
Pred. No.: 1,21e+04  
Score: 37.00  
Percent Similarity: 70.00%  
Best Local Similarity: 70.00%  
Query Match: 3.35%  
DB: 10  
US-09-375-514-22 (1-205) x US-09-245-802-71 (1-40)  
QY 51 SerGlnProGlyHisThrProHisProAla 60  
||||||| ||| ||| |||||

Db 37 ACCGAGCCCCGACACCCGCGCACACCCGCT 8  
RESULT 24  
US-09-734-846-34/c  
; Sequence 34, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-734-846-34  
Alignment Scores:  
Pred. No.: Length: 20  
Score: 6.78e+03  
Percent Similarity: 36.00  
Best Local Similarity: 100.00%  
Conservative: 5  
Query Match: 83.33%  
Mismatch: 1  
Indels: 0  
DB: 0  
Gaps: 0  
US-09-375-514-22 (1-205) x US-09-734-846-34 (1-20)

QY 190 GlnAspAsnGlyGlyTrp 195  
Db 18 CAGGAGACGCGGCTGG 1  
RESULT 25  
US-09-734-847A-45/c  
; Sequence 45, Application US/09734847A  
; Patent No. US20020049173A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Crooke, Stanley T.  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Watt, Jacqueline R.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Freir, Susan  
; APPLICANT: McKay, Robert  
; APPLICANT: Karas, James G.  
; TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation of mRNA  
; FILE REFERENCE: ISPH-0524  
; CURRENT APPLICATION NUMBER: US/09/734,847A  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 20  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-734-847A-45  
Alignment Scores:  
Pred. No.: Length: 20  
Score: 6.78e+03  
Percent Similarity: 36.00  
Best Local Similarity: 100.00%  
Conservative: 5  
Query Match: 83.33%  
Mismatch: 1  
Indels: 0  
DB: 0  
Gaps: 0  
US-09-375-514-22 (1-205) x US-09-734-847A-45 (1-20)  
QY 190 GlnAspAsnGlyGlyTrp 195  
Db 18 CAGGAGACGCGGCTGG 1  
RESULT 26  
US-09-911-904-37/c  
; Sequence 37, Application US/09911904  
; Publication No. US20030096234A1  
; GENERAL INFORMATION:  
; APPLICANT: Fair, Spencer B.  
; APPLICANT: Pickett, Gavin G.  
; APPLICANT: Neft, Robin Eileen  
; APPLICANT: Dunn, II, Robert Thomas  
; TITLE OF INVENTION: CANINE TOXICITY GENES  
; FILE REFERENCE: 400742000200  
; CURRENT APPLICATION NUMBER: US/09/911,904  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US 60/220,057  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 386  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-911-904-37  
Alignment Scores:  
Pred. No.: Length: 25  
Score: 8.82e+03  
Percent Similarity: 36.00  
Best Local Similarity: 85.71%  
Conservative: 5  
Query Match: 71.43%  
Mismatch: 1  
Indels: 0  
DB: 0  
Gaps: 0  
US-09-375-514-22 (1-205) x US-09-911-904-37 (1-25)  
QY 52 GlnProGlyHisThrProHis 58  
Db 24 CGTCCATCTCATACTCCACAT 4  
RESULT 27  
US-09-866-108-4774/c  
; Sequence 4774, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 4774  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4774

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4774 (1-25)

QY 54 GlyHisThrProHisPro 59  
||||| |||||||  
DB 25 GGACATGCTCCTCATCCA 8

RESULT 28  
US-09-866-108-4775/c  
; Sequence 4775, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AROMICA-7  
; CURRENT APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 4775  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4775

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4775 (1-25)

QY 54 GlyHisThrProHisPro 59  
||||| |||||||  
DB 24 GGACATGCTCCTCATCCA 7

RESULT 29  
US-09-866-108-4776/c  
; Sequence 4776, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AROMICA-7  
; CURRENT APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4776 (1-25)

QY 54 GlyHisThProHisPro 59  
Db 23 GGACATGCTCCTCATCCA 6  
RESULT 30  
US-09-866-108-4777/c  
; Sequence 4777, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4777 (1-25)

QY 54 GlyHisThProHisPro 59  
Db 22 GGACATGCTCCTCATCCA 5  
RESULT 31  
US-09-866-108-4778/c  
; Sequence 4778, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 4778  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4778

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservatives: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4778 (1-25)

QY 54 GlyHsthrProHisPro 59  
||||| |||||||  
Db 21 GGACATGCTCTCATCCA 4

## RESULT 32

US-09-866-108-4779/c  
; Sequence 4779, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: ABOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 4779  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4779

Alignment Scores:  
Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservatives: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4779 (1-25)

QY 54 GlyHsthrProHisPro 59  
||||| |||||||  
Db 20 GGACATGCTCTCATCCA 3

## RESULT 33

US-09-866-108-4780/c  
; Sequence 4780, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: ABOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 4780

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-4780

Alignment Scores:

Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4780 (1-25)

QY 54 GlyHISThrProHisPro 59

DB 19 GGACATGCTCCTCATCCA 2

RESULT 34

Sequence 4781, Application US/09866108

Patent No. US20020048800A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharron G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ACOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 15752

SOFTWARE: Acomica Sequence Listing Engine

SEQ ID NO 4781

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-4781

Alignment Scores:

Pred. No.: 8.82e+03 Length: 25  
Score: 36.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4781 (1-25)

QY 54 GlyHISThrProHisPro 59

DB 18 GGACATGCTCCTCATCCA 1

RESULT 35

US-09-817-387-11/c

Sequence 11, Application US/09817387

Patent No. US20010039263A1

GENERAL INFORMATION:

APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin

TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof

FILE REFERENCE: 101195-24

CURRENT APPLICATION NUMBER: US/09/817,387

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: DE 197 20 151.2

PRIOR FILING DATE: 1997-05-02

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotides, linkages between positions 1

OTHER INFORMATION: to 20 are phosphorothioate, linkages between

OTHER INFORMATION: positions 20 to 28 are N3' to N5'

OTHER INFORMATION: phosphoramidates

OTHER INFORMATION: position 28 is modified by a 3'-aminodeoxyribose

OTHER INFORMATION: residue

US-09-817-387-11

Alignment Scores:

Pred. No.: 1.01e+04 Length: 28  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-817-387-11 (1-28)

QY 142 ValAsnTrpGlyArgIle 147

DB 18 GTGAAGTGGGGAGGATT 1

RESULT 36

US-09-949-145-28/c

Sequence 28, Application US/09949145

Patent No. US20020055622A1

GENERAL INFORMATION:

APPLICANT: New York Blood Center

TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and

FILE REFERENCE: Docket 454-31

CURRENT APPLICATION NUMBER: US/09/949,145

CURRENT FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/230660

PRIOR FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.1

SEQ ID NO 28

```
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-949-145-28

Alignment Scores:
Pred. No.: 1.05e+04
Score: 36.00
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Query Match: 3.26%
DB: 10

US-09-375-514-22 (1-205) x US-09-949-145-28 (1-29)

QY 53 ProGlyHisThrProHis 58
Db 28 CCAGCCCAATGCTCCGAC 11

RESULT 37
; Sequence 8, Application US/10245206
; Publication No. US2003007312A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Cantner, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/10245206
; CURRENT FILING DATE: 2002-09-16
; EARLIER APPLICATION NUMBER: US/09/291,129
; EARLIER FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US/09/030,156
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US/08/859,644
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US/08/725,976
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US/08/534,454
; PRIOR FILING DATE: 1995-09-27
; PRIOR APPLICATION NUMBER: US/08/304,657
; PRIOR FILING DATE: 1994-07-07
; PRIOR APPLICATION NUMBER: US/08/146,504
; PRIOR FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-10-245-206-8

Alignment Scores:
Pred. No.: 1.09e+04
Score: 36.00
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Query Match: 3.26%
DB: 9

US-09-375-514-22 (1-205) x US-10-245-206-8 (1-30)

QY 40 ProGlyAlaProAlaProGly 47
Db 28 CCAGCCCAATGCTCCGAC 11

RESULT 38
; Sequence 8, Application US/09291129
; Patent No. US20010014449A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Cantner, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US/09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US/08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US/08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US/08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US/08/708,262
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US/08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US/08/304,657
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US/08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US/08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-291-129-8

Alignment Scores:
Pred. No.: 1.09e+04
Score: 36.00
Percent Similarity: 75.00%
Best Local Similarity: 75.00%
Query Match: 3.26%
DB: 10

US-09-375-514-22 (1-205) x US-09-291-129-8 (1-30)

QY 40 ProGlyAlaProAlaProGly 47
Db 30 CCAGGTGGAGCACCAGCCTGGA 7

RESULT 39
; Sequence 1215, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US/08/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US/08/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
```

```
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-949-145-28

Alignment Scores:
Pred. No.: 1.05e+04
Score: 36.00
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Query Match: 3.26%
DB: 10

US-09-375-514-22 (1-205) x US-09-949-145-28 (1-29)

QY 53 ProGlyHisThrProHis 58
Db 28 CCAGCCCAATGCTCCGAC 11

RESULT 37
; Sequence 8, Application US/10245206
; Publication No. US2003007312A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Cantner, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/10245206
; CURRENT FILING DATE: 2002-09-16
; EARLIER APPLICATION NUMBER: US/09/291,129
; EARLIER FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US/09/030,156
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US/08/859,644
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US/08/725,976
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US/08/534,454
; PRIOR FILING DATE: 1995-09-27
; PRIOR APPLICATION NUMBER: US/08/304,657
; PRIOR FILING DATE: 1994-07-07
; PRIOR APPLICATION NUMBER: US/08/146,504
; PRIOR FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-10-245-206-8

Alignment Scores:
Pred. No.: 1.09e+04
Score: 36.00
Percent Similarity: 83.33%
Best Local Similarity: 83.33%
Query Match: 3.26%
DB: 9

US-09-375-514-22 (1-205) x US-10-245-206-8 (1-30)

QY 40 ProGlyAlaProAlaProGly 47
Db 28 CCAGCCCAATGCTCCGAC 11

RESULT 38
; Sequence 8, Application US/09291129
; Patent No. US20010014449A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Cantner, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US/09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US/08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US/08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US/08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US/08/708,262
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US/08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US/08/304,657
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US/08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US/08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-291-129-8

Alignment Scores:
Pred. No.: 1.09e+04
Score: 36.00
Percent Similarity: 75.00%
Best Local Similarity: 75.00%
Query Match: 3.26%
DB: 10

US-09-375-514-22 (1-205) x US-09-291-129-8 (1-30)

QY 40 ProGlyAlaProAlaProGly 47
Db 30 CCAGGTGGAGCACCAGCCTGGA 7

RESULT 39
; Sequence 1215, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US/08/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US/08/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
```

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1215  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-801-274-1215

Alignment Scores:  
Pred. No.: 1.14e+04 Length: 31  
Score: 36.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-801-274-1215 (1-31)

Qy 72 LeuGlnThrProAlaAlaPro 78  
Db 27 CTACAGACGCGCGGCCCT 7

## RESULT 40

US-09-854-356-15/c  
; Sequence 15, Application US/09854356  
; Patent No. US20020177567A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Gheysen, Dirk  
; APPLICANT: Corixa Corporation  
; APPLICANT: SmithKline Beecham Biologicals S. A.  
; TITLE OF INVENTION: HER-2/neu Fusion Proteins  
; FILE REFERENCE: 014058-009810PC  
; CURRENT APPLICATION NUMBER: US/09/854,356  
; CURRENT FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: US 09/493,480  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,976  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer  
US-09-854-356-15

Alignment Scores:  
Pred. No.: 1.18e+04 Length: 32  
Score: 36.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 0  
Query Match: 3.26% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-09-854-356-15 (1-32)

Qy 185 LeuHlsThrTrpIleGlnAspAsn 192  
Db 26 GTGCACACTTGGGTCCGCAATCA 3

## RESULT 41

US-10-000-512-23/c  
; Sequence 23, Application US/10000512  
; Patent No. US20020164699A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Fernandes, Elma  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME  
; FILE REFERENCE: 15966-556  
; CURRENT APPLICATION NUMBER: US/10/000,512

; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 09/619,252  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/167,785  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER  
US-10-000-512-23

Alignment Scores:  
Pred. No.: 1.31e+04 Length: 35  
Score: 36.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 85.71% Mismatches: 0  
Query Match: 3.26% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x US-10-000-512-23 (1-35)

Qy 40 ProGlyAlaProAlaPro 46  
Db 35 CCCGGGGCTTCCCGTGGCC 15

## RESULT 42

US-09-473-872-31  
; Sequence 31, Application US/09473872  
; Patent No. US20020064876A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoon, Kyonggeun  
; TITLE OF INVENTION: No. US20020064876A1e1 Gene Therapy Methods For The Treatment  
; TITLE OF INVENTION: Disorders  
; FILE REFERENCE: JEFF-Y0001  
; CURRENT APPLICATION NUMBER: US/09/473,872  
; CURRENT FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: COL7A1 gene  
; OTHER INFORMATION: fragment from a normal human  
US-09-473-872-31

Alignment Scores:  
Pred. No.: 1.49e+04 Length: 39  
Score: 36.00 Matches: 6  
Percent Similarity: 60.00% Conservative: 0  
Best Local Similarity: 60.00% Mismatches: 4  
Query Match: 3.26% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-473-872-31 (1-39)

Qy 75 ProAlaAlaProGlyAlaAlaAlaGlyPro 84  
Db 4 CCAGGGGGTCCCGAGCTCCCGGGGGCCCA 33

## RESULT 43

US-09-894-633A-78  
; Sequence 78, Application US/09894633A  
; Patent No. US20020124285A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Malven, Marianne



```

; APPLICANT: Masucci, James
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
; FILE REFERENCE: 38-21(15856)JB
; CURRENT APPLICATION NUMBER: US/09/894,633A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,357
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 09/894,633
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78
; LENGTH: 39
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(39)
; OTHER INFORMATION: synthetic primer sequence
US-09-894-633A-78

Alignment Scores:
Pred. No.: 1.49e+04 Length: 39
Score: 36.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 3.26% Indels: 0
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-894-633A-78 (1-39)
Qy 84 ProAlaLeuSerProValProProVal 92
Db 5 CCAGATCTATTTCCTGTCCTCCCTGTG 31

RESULT 44
US-09-735-363A-2
; Sequence 2, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-2

Alignment Scores:
Pred. No.: 1.09e+04 Length: 27
Score: 35.50 Matches: 6
Percent Similarity: 70.00% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 3.22% Indels: 3
DB: 10 Gaps: 1

US-09-375-514-22 (1-205) x US-09-735-363A-2 (1-27)
Qy 188 TrpIleGlnAspAsnGlyGlyTrpValGly 197
Db 4 TGGGTG-----GGTGGTGGTGGGT 24

RESULT 45
US-09-735-363A-67
; Sequence 67, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-67

Alignment Scores:
Pred. No.: 1.09e+04 Length: 27
Score: 35.50 Matches: 6
Percent Similarity: 70.00% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 3.22% Indels: 3
DB: 10 Gaps: 1

US-09-375-514-22 (1-205) x US-09-735-363A-67 (1-27)
Qy 188 TrpIleGlnAspAsnGlyGlyTrpValGly 197
Db 4 TGGGTG-----GGTGGTGGTGGGT 24

RESULT 46
US-09-866-108-4465/c
; Sequence 4465, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
```

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 4465  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4465

Alignment Scores:  
Pred. No.: 1.12e+04 Length: 25  
Score: 35.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.17% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4465 (1-25)

QY 53 ProglyHistrProHis 58

Db 25 CCAGGGCACCAGCCCAT 8

RESULT 47

US-09-866-108-4466/c  
; Sequence 4466, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 4466  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-4466

Alignment Scores:  
Pred. No.: 1.12e+04 Length: 25  
Score: 35.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.17% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4466 (1-25)

QY 53 ProglyHistrProHis 58

Db 24 CCAGGGCACCAGCCCAT 7

RESULT 48

US-09-866-108-4467/c

; Sequence 4467, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687



Alignment Scores:  
Pred. No.: 1.12e+04 Length: 25  
Score: 35.00 Matches: 5  
Percent Similarity: 83.33% Conservative: 0  
Best Local Similarity: 83.33% Mismatches: 1  
Query Match: 3.17% Indels: 0  
DB: 10 Gaps: 0

US-09-375-514-22 (1-205) x US-09-866-108-4469 (1-25)

QY 53 ProGlyHisThrProHis 58

DB 21 CCAGGGCACCCAGGCCCAT 4

Search completed: May 31, 2003, 23:25:39  
Job time : 134 secs

GenCore version 5.1.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 22:21:35 ; Search time 62 Seconds  
(without alignments)  
1014.012 Million cell updates/sec

Title: US-09-375-514-22  
Perfect score: 1104  
Sequence: 1 MAHAGRTGYDNRREIVMKYIH.....HTWIODNGWGVCASGDVSLG 205

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 551232

Minimum DB seq length: 10  
Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Command line parameters:

-MODEL=frame+pn.model -DEV=xlp  
-Q/cgn2\_1/USPTO.spool/US09375514/runat\_28052003\_165346\_18684/app\_query.fasta\_1.391  
-DB-Issued Patents NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50  
-MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=10 -MAXLEN=40  
-USER=US09375514.@cgn2\_1\_36@runat\_28052003\_165346\_18684 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	66	6.0	33	1	US-07-936-421-15
2	57	5.2	36	1	US-07-936-421-5
3	55	5.0	24	1	US-08-798-897-8
4	55	5.0	24	2	US-08-978-523-8
5	47	4.3	33	1	US-08-217-082A-4
6	47	4.3	33	2	US-08-465-485A-4
7	47	4.3	33	3	US-09-080-285-4
8	47	4.3	33	4	US-09-724-426-4
9	45	4.1	28	1	US-07-936-421-8
10	44	4.0	24	2	US-08-480-994-11
11	44	4.0	24	2	US-08-616-844-11
12	44	4.0	24	2	US-08-599-654-11

Sequence 11, Appl	2	US-08-485-573-11	24	4.0	44
Sequence 11, Appl	3	US-08-944-868A-11	24	4.0	44
Sequence 11, Appl	3	US-08-944-423A-11	24	4.0	44
Sequence 11, Appl	24	US-08-925-743-11	24	4.0	44
Sequence 11, Appl	24	US-08-944-496-11	24	4.0	44
Sequence 11, Appl	24	US-08-925-767-11	24	4.0	44
Sequence 596, App	25	US-08-859-998-596	24	3.8	42
Sequence 596, App	25	US-09-225-928-596	25	3.8	42
Sequence 21, Appl	39	US-08-440-391-21	39	3.8	42
Sequence 21, Appl	39	US-08-908-597A-21	39	3.8	42
Sequence 21, Appl	39	US-09-236-385A-21	39	3.8	42
Sequence 28, Appl	5	PCT-US96-06122-21	39	3.8	42
Sequence 28, Appl	33	US-08-426-819A-28	33	3.7	41
Sequence 6, Appl	36	US-08-427-097-6	36	3.7	41
Sequence 6, Appl	36	US-08-878-957-6	36	3.7	41
Sequence 2, Appl	38	US-08-145-704-2	38	3.7	41
Sequence 2, Appl	38	US-08-987-574-2	38	3.7	41
Sequence 2, Appl	38	US-08-535-168-2	38	3.7	41
Sequence 2, Appl	38	US-09-017-974-2	38	3.7	41
Sequence 2, Appl	38	US-08-682-255A-2	38	3.7	41
Sequence 2, Appl	38	US-09-429-130-2	38	3.7	41
Sequence 10, Appl	5	PCT-US92-03202-10	38	3.7	41
Sequence 11, Appl	5	PCT-US93-08329-11	38	3.7	41
Sequence 2, Appl	38	PCT-US96-11786-2	38	3.7	41
Sequence 10, Appl	27	PCT-US95-06987-10	38	3.6	40
Sequence 8, Appl	35	US-08-497-312-8	35	3.6	40
Sequence 10, Appl	35	US-08-497-312-10	35	3.6	40
Sequence 7, Appl	40	US-08-463-682-7	40	3.6	40
Sequence 110, App	3	US-08-469-318-110	40	3.5	39
Sequence 110, App	3	US-08-468-609A-110	40	3.5	39
Sequence 110, App	4	US-08-446-872A-110	40	3.5	39
Sequence 110, App	4	US-08-762-227A-110	40	3.5	39
Sequence 110, App	5	PCT-US95-01185-110	40	3.5	39
Sequence 2, Appl	30	US-09-485-636-2	40	3.4	38
Sequence 3, Appl	35	PCT-US95-06987-3	35	3.4	38
Sequence 3, Appl	36	US-09-367-750-5	36	3.4	38
Sequence 3, Appl	20	US-08-217-082A-3	36	3.4	38
Sequence 3, Appl	20	US-08-465-485A-3	36	3.4	38
Sequence 3, Appl	20	US-09-080-285-3	36	3.4	38
Sequence 3, Appl	20	US-09-724-426-3	36	3.4	38
Sequence 1, Appl	20	US-09-301-836-1	36	3.4	38
Sequence 10, Appl	28	US-08-340-812-10	36	3.4	38
Sequence 10, Appl	28	US-08-459-064B-10	36	3.4	38
Sequence 10, Appl	28	US-08-460-421A-10	36	3.4	38
Sequence 11, Appl	28	US-08-717-169-11	36	3.4	38
Sequence 10, Appl	28	PCT-US93-00909-10	36	3.4	38
Sequence 1, Appl	38	US-08-145-704-1	38	3.4	38
Sequence 1, Appl	38	US-08-987-574-1	38	3.4	38
Sequence 1, Appl	38	US-08-535-168-1	38	3.4	38
Sequence 1, Appl	38	US-09-017-974-1	38	3.4	38
Sequence 1, Appl	38	US-08-682-255A-1	38	3.4	38
Sequence 1, Appl	38	US-09-429-130-1	38	3.4	38
Sequence 1, Appl	38	PCT-US93-07743-1	38	3.4	38
Sequence 6, Appl	38	PCT-US93-07743-6	38	3.4	38
Sequence 15, Appl	38	PCT-US93-07743-15	38	3.4	38
Sequence 1, Appl	38	PCT-US96-11786-1	38	3.4	38
Sequence 2, Appl	40	US-09-089-594-2	40	3.4	38
Sequence 2, Appl	40	US-08-314-588B-2	40	3.4	38
Sequence 2, Appl	40	US-08-390-878-2	40	3.4	38
Sequence 71, Appl	40	US-08-425-684-71	40	3.4	38
Sequence 71, Appl	40	US-08-675-502-71	40	3.4	38
Sequence 11, Appl	40	US-08-887-674E-11	40	3.4	38
Sequence 34, Appl	20	US-09-167-921-34	40	3.3	36
Sequence 45, Appl	20	US-09-277-020-45	40	3.3	36
Sequence 34, Appl	20	US-09-323-743-34	40	3.3	36
Sequence 1, Appl	20	US-09-445-486-1	40	3.3	36
Sequence 3, Appl	20	US-09-445-486-3	40	3.3	36
Sequence 4, Appl	23	US-07-936-421-4	40	3.3	36
Sequence 8, Appl	30	US-09-291-129-8	40	3.3	36
Sequence 81, Appl	30	PCT-US95-10973A-80	40	3.3	36
Sequence 81, Appl	30	PCT-US95-10973A-81	40	3.3	36
Sequence 2, Appl	32	US-07-990-965-2	40	3.3	36
Sequence 7, Appl	35	US-08-340-045-7	40	3.3	36

c 85	36	3.3	35	3	US-08-871-302A-7	Sequence 7, Appl	c 159	34	3.1	40	1	US-08-038-071-1	Sequence 1, Appl
c 86	36	3.3	38	1	US-07-977-434-22	Sequence 22, Appl	c 160	34	3.1	40	2	US-08-461-286-1	Sequence 1, Appl
c 87	36	3.3	38	1	US-08-458-819-22	Sequence 22, Appl	c 161	34	3.1	40	5	PCT-US92-02854-1	Sequence 1, Appl
c 88	36	3.3	38	4	US-09-552-322-35	Sequence 35, Appl	c 162	34	3.1	40	6	5498600-22	Patent No. 5498600
c 89	36	3.3	38	5	PCT-US91-070325-22	Sequence 22, Appl	c 163	33.5	3.0	33	4	US-09-091-219-14	Sequence 14, Appl
c 90	36	3.3	38	4	US-08-973-131-29	Sequence 29, Appl	c 164	33.5	3.0	36	3	US-08-718-904-66	Sequence 38, Appl
c 91	36	3.3	39	4	US-09-485-737B-6	Sequence 6, Appl	c 165	33.5	3.0	36	3	PCT-US95-10973A-38	Patent No. 5520913
c 92	36	3.3	40	4	US-08-145-704-19	Sequence 19, Appl	c 166	33.5	3.0	36	6	US-08-987-574-48	Sequence 48, Appl
c 93	35.5	3.2	26	1	US-08-535-168-19	Sequence 19, Appl	c 167	33	3.0	16	3	US-08-987-574-48	Sequence 48, Appl
c 94	35.5	3.2	26	3	US-08-987-574-19	Sequence 19, Appl	c 168	33	3.0	16	4	US-08-535-168-48	Sequence 48, Appl
c 95	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 169	33	3.0	16	4	US-09-017-974-48	Sequence 48, Appl
c 96	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 170	33	3.0	16	4	US-08-682-255A-48	Sequence 48, Appl
c 97	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 171	33	3.0	16	4	US-09-429-130-48	Sequence 48, Appl
c 98	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 172	33	3.0	16	4	US-09-429-130-48	Sequence 48, Appl
c 99	35.5	3.2	26	4	US-08-535-168-19	Sequence 19, Appl	c 173	33	3.0	16	5	PCT-US96-11786-48	Sequence 48, Appl
c 100	35.5	3.2	27	1	US-08-145-704-14	Sequence 14, Appl	c 174	33	3.0	17	1	US-08-145-704-33	Sequence 33, Appl
c 101	35.5	3.2	27	3	US-08-987-574-14	Sequence 14, Appl	c 175	33	3.0	17	3	US-08-987-574-33	Sequence 33, Appl
c 102	35.5	3.2	27	4	US-08-535-168-14	Sequence 14, Appl	c 176	33	3.0	17	3	US-08-987-574-33	Sequence 33, Appl
c 103	35.5	3.2	27	4	US-09-017-974-14	Sequence 14, Appl	c 177	33	3.0	17	3	US-08-987-574-46	Sequence 46, Appl
c 104	35.5	3.2	27	4	US-08-682-255A-14	Sequence 14, Appl	c 178	33	3.0	17	4	US-08-535-168-33	Sequence 33, Appl
c 105	35.5	3.2	27	4	US-09-429-130-14	Sequence 14, Appl	c 179	33	3.0	17	4	US-08-535-168-46	Sequence 46, Appl
c 106	35.5	3.2	27	5	PCT-US96-11786-14	Sequence 14, Appl	c 180	33	3.0	17	4	US-09-017-974-33	Sequence 33, Appl
c 107	35	3.2	19	4	US-09-031-962D-13	Sequence 13, Appl	c 181	33	3.0	17	4	US-09-017-974-46	Sequence 46, Appl
c 108	35	3.2	20	4	US-09-248-568-4	Sequence 4, Appl	c 182	33	3.0	17	4	US-09-017-974-59	Sequence 59, Appl
c 109	35	3.2	27	4	US-08-551-211-2	Sequence 2, Appl	c 183	33	3.0	17	4	US-09-017-974-60	Sequence 60, Appl
c 110	35	3.2	30	4	US-09-342-143-18	Sequence 18, Appl	c 184	33	3.0	17	4	US-09-017-974-68	Sequence 68, Appl
c 111	35	3.2	30	4	US-09-195-106-16	Sequence 16, Appl	c 185	33	3.0	17	4	US-09-017-974-72	Sequence 72, Appl
c 112	35	3.2	30	4	US-09-195-106-19	Sequence 19, Appl	c 186	33	3.0	17	4	US-09-017-974-75	Sequence 75, Appl
c 113	35	3.2	30	4	US-09-549-564-7	Sequence 7, Appl	c 187	33	3.0	17	4	US-09-017-974-79	Sequence 79, Appl
c 114	35	3.2	32	1	US-08-021-608D-14	Sequence 14, Appl	c 188	33	3.0	17	4	US-09-017-974-87	Sequence 87, Appl
c 115	35	3.2	32	1	US-08-726-160-14	Sequence 14, Appl	c 189	33	3.0	17	4	US-08-682-255A-33	Sequence 33, Appl
c 116	35	3.2	36	2	US-08-454-028-8	Sequence 8, Appl	c 190	33	3.0	17	4	US-08-682-255A-46	Sequence 46, Appl
c 117	35	3.2	36	2	US-08-833-963C-5	Sequence 5, Appl	c 191	33	3.0	17	4	US-08-682-255A-58	Sequence 58, Appl
c 118	35	3.2	36	5	PCT-US94-05388-8	Sequence 8, Appl	c 192	33	3.0	17	4	US-08-682-255A-59	Sequence 59, Appl
c 119	35	3.2	36	5	PCT-US96-07496-8	Sequence 8, Appl	c 193	33	3.0	17	4	US-08-682-255A-60	Sequence 60, Appl
c 120	35	3.2	38	3	US-08-863-813A-49	Sequence 49, Appl	c 194	33	3.0	17	4	US-08-682-255A-68	Sequence 68, Appl
c 121	35	3.2	39	4	US-09-143-634-10	Sequence 10, Appl	c 195	33	3.0	17	4	US-08-682-255A-72	Sequence 72, Appl
c 122	35	3.2	39	4	US-09-593-995-8	Sequence 8, Appl	c 196	33	3.0	17	4	US-08-682-255A-75	Sequence 75, Appl
c 123	34	3.1	19	1	US-07-936-421-14	Sequence 14, Appl	c 197	33	3.0	17	4	US-08-682-255A-79	Sequence 79, Appl
c 124	34	3.1	20	4	US-09-277-020-64	Sequence 64, Appl	c 198	33	3.0	17	4	US-08-682-255A-87	Sequence 87, Appl
c 125	34	3.1	20	4	US-08-545-809A-86	Sequence 86, Appl	c 199	33	3.0	17	4	US-09-429-130-33	Sequence 33, Appl
c 126	34	3.1	21	3	US-07-936-421-6	Sequence 6, Appl	c 200	33	3.0	17	4	US-09-429-130-46	Sequence 46, Appl
c 127	34	3.1	22	1	US-08-616-732A-15	Sequence 15, Appl	c 201	33	3.0	17	4	US-09-429-130-58	Sequence 58, Appl
c 128	34	3.1	22	1	US-08-616-732A-16	Sequence 16, Appl	c 202	33	3.0	17	4	US-09-429-130-59	Sequence 59, Appl
c 129	34	3.1	22	3	US-09-037-742B-15	Sequence 15, Appl	c 203	33	3.0	17	4	US-09-429-130-68	Sequence 68, Appl
c 130	34	3.1	22	3	US-09-037-742B-16	Sequence 16, Appl	c 204	33	3.0	17	4	US-09-429-130-72	Sequence 72, Appl
c 131	34	3.1	22	3	US-08-331-616A-16	Sequence 16, Appl	c 205	33	3.0	17	4	US-09-429-130-75	Sequence 75, Appl
c 132	34	3.1	30	2	US-08-712-610-6	Sequence 6, Appl	c 206	33	3.0	17	4	US-09-429-130-87	Sequence 87, Appl
c 133	34	3.1	30	3	US-09-309-423-6	Sequence 6, Appl	c 207	33	3.0	17	4	PCT-US96-11786-33	Sequence 33, Appl
c 134	34	3.1	30	4	US-09-052-919-51	Sequence 51, Appl	c 208	33	3.0	17	5	PCT-US96-11786-46	Sequence 46, Appl
c 135	34	3.1	31	1	US-08-530-492-137	Sequence 137, App	c 209	33	3.0	17	5	PCT-US96-11786-46	Sequence 46, Appl
c 136	34	3.1	31	4	US-08-906-517-137	Sequence 137, App	c 210	33	3.0	18	1	US-08-145-704-3	Sequence 3, Appl
c 137	34	3.1	32	2	US-08-174-672D-49	Sequence 49, Appl	c 211	33	3.0	18	1	US-08-145-704-31	Sequence 31, Appl
c 138	34	3.1	33	1	US-08-424-268-2	Sequence 2, Appl	c 212	33	3.0	18	1	US-08-145-704-32	Sequence 32, Appl
c 139	34	3.1	33	2	US-08-967-101-142	Sequence 142, App	c 213	33	3.0	18	1	US-08-319-492B-749	Sequence 749, App
c 140	34	3.1	33	2	US-08-592-541-142	Sequence 142, App	c 214	33	3.0	18	3	US-08-987-574-3	Sequence 3, Appl
c 141	34	3.1	33	2	US-09-124-698-142	Sequence 142, App	c 215	33	3.0	18	3	US-08-987-574-31	Sequence 31, Appl
c 142	34	3.1	33	3	US-09-124-698-142	Sequence 142, App	c 216	33	3.0	18	3	US-08-987-574-32	Sequence 32, Appl
c 143	34	3.1	33	4	US-09-127-480-142	Sequence 142, App	c 217	33	3.0	18	4	US-08-535-168-3	Sequence 3, Appl
c 144	34	3.1	33	4	US-07-987-264-26	Sequence 26, App	c 218	33	3.0	18	4	US-08-535-168-31	Sequence 31, Appl
c 145	34	3.1	33	4	US-08-496-841C-142	Sequence 142, App	c 219	33	3.0	18	4	US-08-535-168-32	Sequence 32, Appl
c 146	34	3.1	33	5	PCT-US93-10442-2	Sequence 2, Appl	c 220	33	3.0	18	4	US-09-017-974-3	Sequence 3, Appl
c 147	34	3.1	34	1	US-08-373-124A-31	Sequence 31, Appl	c 221	33	3.0	18	4	US-09-017-974-31	Sequence 31, Appl
c 148	34	3.1	34	1	US-08-435-628-31	Sequence 31, Appl	c 222	33	3.0	18	4	US-09-017-974-32	Sequence 32, Appl
c 149	34	3.1	36	1	US-08-352-179-15	Sequence 15, Appl	c 223	33	3.0	18	4	US-08-682-255A-3	Sequence 3, Appl
c 150	34	3.1	36	1	US-08-352-179-16	Sequence 16, Appl	c 224	33	3.0	18	4	US-08-682-255A-31	Sequence 31, Appl
c 151	34	3.1	38	1	US-09-499-884-12	Sequence 12, Appl	c 225	33	3.0	18	4	US-08-682-255A-32	Sequence 32, Appl
c 152	34	3.1	39	1	US-08-737-597-7	Sequence 7, Appl	c 226	33	3.0	18	4	US-09-429-130-3	Sequence 3, Appl
c 153	34	3.1	39	2	US-09-057-762-5	Sequence 5, Appl	c 227	33	3.0	18	4	US-09-429-130-31	Sequence 31, Appl
c 154	34	3.1	39	3	US-08-326-119A-5	Sequence 5, Appl	c 228	33	3.0	18	4	US-09-429-130-32	Sequence 32, Appl
c 155	34	3.1	39	4	US-09-513-783A-147	Sequence 147, App	c 229	33	3.0	18	5	PCT-US96-11786-3	Sequence 3, Appl
c 156	34	3.1	39	4	US-09-538-709-36	Sequence 36, Appl	c 230	33	3.0	18	5	PCT-US96-11786-31	Sequence 31, Appl
c 157	34	3.1	39	4	US-09-538-709-37	Sequence 37, Appl	c 231	33	3.0	18	5	PCT-US96-11786-32	Sequence 32, Appl

c 232	33	3.0	20	3	US-08-850-347-9	Sequence 9, Appli	305	33	3.0	40	1	US-08-199-507B-49	Sequence 49, Appli
c 233	33	3.0	20	3	US-08-990-065-9	Sequence 9, Appli	306	33	3.0	40	1	US-08-441-828-49	Sequence 49, Appli
c 234	33	3.0	22	1	US-08-367-227-4	Sequence 4, Appli	307	33	3.0	40	2	US-08-425-684-4	Sequence 4, Appli
c 235	33	3.0	22	2	US-08-531-070A-12	Sequence 12, Appli	308	33	3.0	40	2	US-08-675-502-4	Sequence 4, Appli
c 236	33	3.0	23	1	US-08-052-404-14	Sequence 14, Appli	309	32.5	2.9	34	4	US-09-440-621-9	Sequence 9, Appli
c 237	33	3.0	23	1	US-08-479-156-14	Sequence 14, Appli	310	32.5	2.9	37	4	US-08-433-505-1	Sequence 1, Appli
c 238	33	3.0	26	3	US-08-224-981-2	Sequence 2, Appli	311	32.5	2.9	37	3	US-08-264-996-1	Sequence 1, Appli
c 239	33	3.0	26	3	US-09-047-347-29	Sequence 29, Appli	312	32.5	2.9	37	3	US-08-870-730-1	Sequence 1, Appli
c 240	33	3.0	27	1	US-08-145-704-34	Sequence 34, Appli	313	32	2.9	18	1	US-08-217-082A-17	Sequence 17, Appli
c 241	33	3.0	27	1	US-08-440-391-27	Sequence 27, Appli	314	32	2.9	18	2	US-08-465-485A-17	Sequence 17, Appli
c 242	33	3.0	27	1	US-08-434-411-54	Sequence 54, Appli	315	32	2.9	18	2	US-08-465-485A-24	Sequence 24, Appli
c 243	33	3.0	27	1	US-08-434-402-54	Sequence 54, Appli	316	32	2.9	18	3	US-09-080-285-17	Sequence 17, Appli
c 244	33	3.0	27	1	US-08-783-288-54	Sequence 54, Appli	317	32	2.9	18	3	US-09-080-285-17	Sequence 17, Appli
c 245	33	3.0	27	1	US-08-908-597A-27	Sequence 27, Appli	318	32	2.9	18	3	US-09-249-730-218	Sequence 218, App
c 246	33	3.0	27	2	US-08-890-640-54	Sequence 54, Appli	319	32	2.9	18	3	US-09-118-220-1	Sequence 1, Appli
c 247	33	3.0	27	3	US-08-987-574-34	Sequence 34, Appli	320	32	2.9	18	4	US-08-738-652-55	Sequence 55, Appli
c 248	33	3.0	27	4	US-08-535-168-34	Sequence 34, Appli	321	32	2.9	18	4	US-09-030-701-27	Sequence 27, Appli
c 249	33	3.0	27	4	US-09-253-398A-94	Sequence 94, Appli	322	32	2.9	18	4	US-09-286-098-59	Sequence 59, Appli
c 250	33	3.0	27	4	US-09-236-385A-27	Sequence 27, Appli	323	32	2.9	18	4	US-09-286-098-104	Sequence 104, App
c 251	33	3.0	27	4	US-09-017-974-34	Sequence 34, Appli	324	32	2.9	18	4	US-08-960-774-45	Sequence 45, Appli
c 252	33	3.0	27	4	US-08-682-255A-34	Sequence 34, Appli	325	32	2.9	18	4	US-09-078-954-14	Sequence 14, Appli
c 253	33	3.0	27	4	US-09-429-130-34	Sequence 34, Appli	326	32	2.9	18	4	US-09-325-193A-51	Sequence 51, Appli
c 254	33	3.0	27	5	PCT-US96-06122-27	Sequence 27, Appli	327	32	2.9	18	4	US-09-724-426-17	Sequence 17, Appli
c 255	33	3.0	27	5	PCT-US96-11786-34	Sequence 34, Appli	328	32	2.9	18	4	US-09-191-170-53	Sequence 53, Appli
c 256	33	3.0	27	6	5194592-79	Patent No. 5194592	329	32	2.9	18	4	US-09-109-663-72	Sequence 72, Appli
c 257	33	3.0	28	4	US-09-521-668B-7	Sequence 7, Appli	330	32	2.9	20	4	US-09-082-649B-60	Sequence 60, Appli
c 258	33	3.0	29	2	US-08-860-882A-4	Sequence 4, Appli	331	32	2.9	20	4	US-09-689-255C-12	Sequence 12, Appli
c 259	33	3.0	29	3	US-08-840-062-12	Sequence 12, Appli	332	32	2.9	20	4	US-08-318-837-38	Sequence 38, Appli
c 260	33	3.0	30	1	US-08-384-708A-127	Sequence 127, App	333	32	2.9	21	2	US-08-867-230A-7	Sequence 7, Appli
c 261	33	3.0	30	2	US-08-117-952-630	Sequence 630, App	334	32	2.9	21	2	US-08-778-794A-145	Sequence 145, App
c 262	33	3.0	30	2	US-08-766-439-107	Sequence 107, App	335	32	2.9	25	4	US-09-341-399-42	Sequence 42, Appli
c 263	33	3.0	30	2	US-08-812-102-11	Sequence 11, Appli	336	32	2.9	25	4	US-08-410-804-13	Sequence 13, Appli
c 264	33	3.0	31	1	US-07-988-194A-19	Sequence 19, Appli	337	32	2.9	27	1	US-08-607-269-8	Sequence 8, Appli
c 265	33	3.0	31	1	US-08-258-152-21	Sequence 21, Appli	338	32	2.9	27	1	US-08-525-742-35	Sequence 35, Appli
c 266	33	3.0	31	1	US-08-076-298A-21	Sequence 21, Appli	339	32	2.9	27	1	US-08-525-742-35	Sequence 35, Appli
c 267	33	3.0	31	2	US-08-438-582-21	Sequence 21, Appli	340	32	2.9	27	1	PCT-US95-04600-8	Sequence 8, Appli
c 268	33	3.0	31	2	US-09-266-596-21	Sequence 21, Appli	341	32	2.9	27	1	US-08-859-998-208	Sequence 208, App
c 269	33	3.0	31	4	US-08-479-737-19	Sequence 19, Appli	342	32	2.9	27	2	US-08-023-082A-92	Sequence 92, App
c 270	33	3.0	31	4	US-08-475-442A-19	Sequence 19, Appli	343	32	2.9	27	2	US-09-023-082A-114	Sequence 114, App
c 271	33	3.0	31	6	5492811-8	Patent No. 5492811	344	32	2.9	27	5	US-09-218-44-13	Sequence 13, Appli
c 272	33	3.0	32	4	US-08-623-428D-26	Sequence 26, Appli	345	32	2.9	28	2	US-09-225-928-208	Sequence 208, App
c 273	33	3.0	32	1	US-08-061-889-4	Sequence 4, Appli	346	32	2.9	28	2	US-09-225-928-500	Sequence 500, App
c 274	33	3.0	33	1	US-08-462-611-4	Sequence 4, Appli	347	32	2.9	28	2	US-09-038-227-40	Sequence 40, Appli
c 275	33	3.0	33	1	US-08-846-012A-14	Sequence 14, Appli	348	32	2.9	28	3	US-08-766-439-106	Sequence 106, App
c 276	33	3.0	33	2	US-09-100-297-14	Sequence 14, Appli	349	32	2.9	28	3	US-08-484-257-6	Sequence 6, Appli
c 277	33	3.0	33	4	US-08-623-428D-8	Sequence 8, Appli	350	32	2.9	28	4	US-08-489-269-1	Sequence 1, Appli
c 278	33	3.0	33	5	PCT-US94-05378-4	Sequence 4, Appli	351	32	2.9	28	4	US-08-457-254-17	Sequence 17, Appli
c 279	33	3.0	34	4	US-09-449-218D-41	Sequence 41, Appli	352	32	2.9	28	4	US-08-297-395-44	Sequence 44, Appli
c 280	33	3.0	34	4	US-09-506-768-14	Sequence 14, Appli	353	32	2.9	28	4	US-08-235-836C-2	Sequence 2, Appli
c 281	33	3.0	34	4	US-08-742-755A-33	Sequence 33, Appli	354	32	2.9	28	4	US-09-052-919-50	Sequence 50, Appli
c 282	33	3.0	35	2	US-08-881-037-109	Sequence 109, App	355	32	2.9	30	5	PCT-US94-08806-6	Sequence 6, Appli
c 283	33	3.0	35	3	US-09-226-683-33	Sequence 33, Appli	356	32	2.9	30	5	PCT-US95-01775-6	Sequence 6, Appli
c 284	33	3.0	35	4	US-09-035-183-33	Sequence 33, Appli	357	32	2.9	30	5	US-08-136-119-5	Sequence 55, Appli
c 285	33	3.0	35	4	US-09-232-278A-19	Sequence 19, Appli	358	32	2.9	30	5	US-08-946-914-55	Sequence 43, Appli
c 286	33	3.0	36	4	US-08-327-874A-28	Sequence 28, Appli	359	32	2.9	30	5	US-09-390-326-1	Sequence 1, Appli
c 287	33	3.0	36	5	PCT-US94-09700-28	Sequence 28, Appli	360	32	2.9	30	5	US-09-529-279-29	Sequence 29, Appli
c 288	33	3.0	37	1	US-08-145-704-35	Sequence 35, Appli	361	32	2.9	31	3	US-09-656-450-55	Sequence 55, Appli
c 289	33	3.0	37	3	US-08-987-574-35	Sequence 35, Appli	362	32	2.9	31	3	US-08-426-819A-25	Sequence 25, Appli
c 290	33	3.0	37	4	US-08-535-168-35	Sequence 35, Appli	363	32	2.9	31	3	US-09-370-368-1	Sequence 1, Appli
c 291	33	3.0	37	4	US-09-344-700-33	Sequence 33, Appli	364	32	2.9	31	4	US-08-938-835A-43	Sequence 29, Appli
c 292	33	3.0	37	4	US-09-017-974-35	Sequence 35, Appli	365	32	2.9	31	4	US-09-329-279-29	Sequence 29, Appli
c 293	33	3.0	37	4	US-08-682-455A-35	Sequence 35, Appli	366	32	2.9	31	4	US-09-656-450-55	Sequence 55, Appli
c 294	33	3.0	37	4	US-09-429-130-35	Sequence 35, Appli	367	32	2.9	31	4	US-08-426-819A-25	Sequence 25, Appli
c 295	33	3.0	37	5	PCT-US96-11786-35	Sequence 35, Appli	368	32	2.9	31	4	US-09-370-368-1	Sequence 1, Appli
c 296	33	3.0	38	3	US-08-863-813A-50	Sequence 3, Appli	369	32	2.9	31	4	US-08-203-905B-12	Sequence 12, Appli
c 297	33	3.0	38	3	US-08-951-083-337	Sequence 337, App	370	32	2.9	31	4	US-08-053-131-117	Sequence 117, App
c 298	33	3.0	38	3	US-08-556-978B-64	Sequence 64, Appli	371	32	2.9	31	4	US-08-645-641-117	Sequence 117, App
c 299	33	3.0	39	4	US-08-526-542-8	Sequence 8, Appli	372	32	2.9	32	4		
c 300	33	3.0	39	4	US-09-480-718-33	Sequence 33, Appli	373	32	2.9	32	4		
c 301	33	3.0	40	1	US-07-949-488A-6	Sequence 6, Appli	374	32	2.9	32	4		
c 302	33	3.0					375	32	2.9	32	4		
c 303	33	3.0					376	32	2.9	32	4		
c 304	33	3.0					377	32	2.9	32	4		

c 378	32	2, 9	33	1	US-07-853-408B-117	Sequence 117, App	c 451	32	2, 9	40	4	US-09-150-864A-13	Sequence 13, Appl
c 379	32	2, 9	33	1	US-08-096-762-117	Sequence 117, App	c 452	32	2, 9	40	4	US-09-327-874A-33	Sequence 33, Appl
c 380	32	2, 9	33	2	US-08-676-279-8	Sequence 8, Appl	c 453	32	2, 9	40	4	US-09-622-540A-15	Sequence 15, Appl
c 381	32	2, 9	33	2	US-08-308-865-117	Sequence 117, App	c 454	32	2, 9	40	4	US-09-622-540A-15	Sequence 15, Appl
c 382	32	2, 9	33	2	US-08-476-176B-46	Sequence 46, Appl	c 455	32	2, 9	40	4	US-09-622-540A-15	Sequence 15, Appl
c 383	32	2, 9	33	2	US-08-672-215-2	Sequence 2, Appl	c 456	32	2, 9	40	4	PCT-US94-09700-33	Sequence 33, Appl
c 384	32	2, 9	33	3	US-08-127-721A-46	Sequence 46, Appl	c 457	31, 5	2, 9	36	3	US-08-485-133-75	Sequence 75, Appl
c 385	32	2, 9	33	3	US-08-485-245A-46	Sequence 46, Appl	c 458	31, 5	2, 9	36	3	US-08-830-58	Sequence 58, Appl
c 386	32	2, 9	33	3	US-08-621-841-12	Sequence 12, Appl	c 459	31	2, 8	20	1	US-07-936-421-12	Sequence 12, Appl
c 387	32	2, 9	33	3	US-08-839-624-34	Sequence 34, Appl	c 460	31	2, 8	20	1	US-07-940-242A-94	Sequence 94, Appl
c 388	32	2, 9	33	4	US-09-042-353-309	Sequence 309, App	c 461	31	2, 8	20	1	US-07-940-242A-96	Sequence 96, Appl
c 389	32	2, 9	33	4	US-08-758-417A-157	Sequence 157, App	c 462	31	2, 8	20	1	US-07-940-242A-99	Sequence 99, Appl
c 390	32	2, 9	33	4	US-09-150-812-34	Sequence 34, Appl	c 463	31	2, 8	20	1	US-08-405-702A-13	Sequence 13, Appl
c 391	32	2, 9	33	4	US-09-249-585A-11	Sequence 11, Appl	c 464	31	2, 8	20	4	US-09-167-921-29	Sequence 29, Appl
c 392	32	2, 9	33	5	PCT-US92-10983-117	Sequence 117, App	c 465	31	2, 8	20	4	US-09-490-692-121	Sequence 121, App
c 393	32	2, 9	34	1	US-08-318-193-54	Sequence 54, Appl	c 466	31	2, 8	20	4	US-09-323-743-29	Sequence 29, Appl
c 394	32	2, 9	34	1	US-08-373-124A-32	Sequence 32, Appl	c 467	31	2, 8	20	5	PCT-US95-00593-1	Sequence 1, Appl
c 395	32	2, 9	34	1	US-08-435-628-32	Sequence 32, Appl	c 468	31	2, 8	21	4	US-08-927-219-14	Sequence 14, Appl
c 396	32	2, 9	34	3	US-09-067-089-5	Sequence 5, Appl	c 469	31	2, 8	21	4	US-09-318-191-2	Sequence 2, Appl
c 397	32	2, 9	34	4	US-09-136-574A-11	Sequence 11, Appl	c 470	31	2, 8	21	4	US-09-701-685-4	Sequence 4, Appl
c 398	32	2, 9	35	1	US-08-091-569-3	Sequence 3, Appl	c 471	31	2, 8	22	2	US-08-389-564B-34	Sequence 34, Appl
c 399	32	2, 9	35	1	US-08-203-078A-2	Sequence 2, Appl	c 472	31	2, 8	22	2	US-09-066-597-23	Sequence 23, Appl
c 400	32	2, 9	35	2	US-08-217-082A-2	Sequence 2, Appl	c 473	31	2, 8	22	3	US-08-466-047B-34	Sequence 34, Appl
c 401	32	2, 9	35	2	US-08-465-485A-2	Sequence 2, Appl	c 474	31	2, 8	22	3	US-08-247-629-11	Sequence 11, Appl
c 402	32	2, 9	35	2	US-08-822-238-3	Sequence 2, Appl	c 475	31	2, 8	23	4	US-09-115-446-10	Sequence 10, Appl
c 403	32	2, 9	35	3	US-09-080-285-2	Sequence 2, Appl	c 476	31	2, 8	23	4	US-08-513-974B-228	Sequence 228, App
c 404	32	2, 9	35	3	US-08-892-747-11	Sequence 11, Appl	c 477	31	2, 8	24	3	US-08-811-492-41	Sequence 41, Appl
c 405	32	2, 9	35	4	US-09-724-426-2	Sequence 2, Appl	c 478	31	2, 8	24	3	US-09-010-809-16	Sequence 16, Appl
c 406	32	2, 9	36	1	US-08-690-457-1	Sequence 1, Appl	c 479	31	2, 8	25	3	US-09-001-472-7	Sequence 7, Appl
c 407	32	2, 9	36	2	US-08-811-028-24	Sequence 24, Appl	c 480	31	2, 8	25	4	US-09-494-407-2	Sequence 2, Appl
c 408	32	2, 9	36	2	US-08-811-028-25	Sequence 25, Appl	c 481	31	2, 8	25	5	PCT-US96-10545A-41	Sequence 41, Appl
c 409	32	2, 9	36	3	US-08-718-904-66	Sequence 66, Appl	c 482	31	2, 8	26	1	US-08-233-030-46	Sequence 22, Appl
c 410	32	2, 9	36	3	US-08-983-035A-20	Sequence 20, Appl	c 483	31	2, 8	26	2	US-08-887-798-22	Sequence 3, Appl
c 411	32	2, 9	36	5	PCT-US95-10973A-38	Sequence 38, Appl	c 484	31	2, 8	26	4	US-08-952-981A-33	Sequence 28, Appl
c 412	32	2, 9	37	1	US-08-150-331-9	Sequence 9, Appl	c 485	31	2, 8	26	5	PCT-US92-08094-28	Sequence 20, Appl
c 413	32	2, 9	37	1	US-08-150-331-30	Sequence 30, Appl	c 486	31	2, 8	27	1	US-07-643-734C-20	Sequence 17, Appl
c 414	32	2, 9	37	4	US-09-082-649B-49	Sequence 49, Appl	c 487	31	2, 8	27	2	US-08-500-857A-17	Sequence 20, Appl
c 415	32	2, 9	38	1	US-08-145-704-4	Sequence 4, Appl	c 488	31	2, 8	27	3	US-08-439-009A-20	Sequence 36, Appl
c 416	32	2, 9	38	1	US-08-384-708A-188	Sequence 188, App	c 489	31	2, 8	27	3	US-08-567-200A-36	Sequence 39, Appl
c 417	32	2, 9	38	1	US-08-104-072B-34	Sequence 34, Appl	c 490	31	2, 8	27	3	US-08-691-794-39	Sequence 16, Appl
c 418	32	2, 9	38	1	US-08-642-255-2	Sequence 22, Appl	c 491	31	2, 8	27	4	US-08-623-428D-16	Sequence 25, Appl
c 419	32	2, 9	38	2	US-08-607-519-2	Sequence 2, Appl	c 492	31	2, 8	27	4	US-08-623-428D-25	Sequence 17, Appl
c 420	32	2, 9	38	2	US-08-857-946-117	Sequence 117, App	c 493	31	2, 8	27	4	US-09-098-628-17	Sequence 21, Appl
c 421	32	2, 9	38	3	US-08-970-740-117	Sequence 117, App	c 494	31	2, 8	28	4	PCT-US91-02186-21	Sequence 10, Appl
c 422	32	2, 9	38	3	US-08-475-411A-53	Sequence 53, Appl	c 495	31	2, 8	28	5	US-09-064-703B-10	Sequence 16, Appl
c 423	32	2, 9	38	3	US-08-987-574-4	Sequence 4, Appl	c 496	31	2, 8	29	1	US-08-683-839B-10	Sequence 21, Appl
c 424	32	2, 9	38	3	US-08-968-563-47	Sequence 47, Appl	c 497	31	2, 8	29	3	US-09-064-703B-16	Sequence 16, Appl
c 425	32	2, 9	38	4	US-08-969-683A-47	Sequence 53, Appl	c 498	31	2, 8	29	4	US-08-638-931-6	Sequence 6, Appl
c 426	32	2, 9	38	4	US-08-478-029A-53	Sequence 4, Appl	c 499	31	2, 8	30	1	US-08-279-058B-43	Sequence 43, Appl
c 427	32	2, 9	38	4	US-08-535-168-4	Sequence 4, Appl	c 500	31	2, 8				
c 428	32	2, 9	38	4	US-09-017-974-4	Sequence 4, Appl							
c 429	32	2, 9	38	4	US-08-682-255A-4	Sequence 4, Appl							
c 430	32	2, 9	38	4	US-09-429-130-4	Sequence 4, Appl							
c 431	32	2, 9	38	5	PCT-US96-11786-4	Sequence 7, Appl							
c 432	32	2, 9	39	1	US-08-456-840-7	Sequence 7, Appl							
c 433	32	2, 9	39	1	US-08-530-492-101	Sequence 101, App							
c 434	32	2, 9	39	1	US-08-266-407A-7	Sequence 7, Appl							
c 435	32	2, 9	39	2	US-08-892-544-7	Sequence 47, Appl							
c 436	32	2, 9	39	3	US-08-968-563-47	Sequence 47, Appl							
c 437	32	2, 9	39	3	US-08-969-683A-47	Sequence 17, Appl							
c 438	32	2, 9	39	3	US-09-136-605-17	Sequence 101, App							
c 439	32	2, 9	39	4	US-08-906-517-101	Sequence 12, Appl							
c 440	32	2, 9	39	4	US-08-804-166-12	Sequence 12, Appl							
c 441	32	2, 9	39	4	US-08-910-991-12	Sequence 19, Appl							
c 442	32	2, 9	39	4	US-09-297-928-19	Sequence 13, Appl							
c 443	32	2, 9	40	1	US-08-236-918A-13	Sequence 94, Appl							
c 444	32	2, 9	40	2	US-08-425-684-94	Sequence 38, Appl							
c 445	32	2, 9	40	2	US-08-628-422-38	Sequence 94, Appl							
c 446	32	2, 9	40	2	US-08-675-502-94	Sequence 36, Appl							
c 447	32	2, 9	40	4	US-09-416-050A-36	Sequence 36, Appl							
c 448	32	2, 9	40	4	US-09-664-800-36	Sequence 36, Appl							
c 449	32	2, 9	40	4	US-09-665-309-36	Sequence 36, Appl							
c 450	32	2, 9	40	4	US-09-661-569-36	Sequence 36, Appl							

ALIGNMENTS

RESULT 1  
US-07-936-421-15  
; Sequence 15, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TREATMENT OF DISEASES CAUSED  
; BY EXPRESSION OF THE BCL-2  
; TITLE OF INVENTION:  
; TITLE OF INVENTION: GENE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017



COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/936,421  
FILING DATE: 19920826  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 197/243  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-936-421-15

Alignment Scores:  
Pred. No.: 29.1 Length: 36  
Score: 66.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.98% Indels: 0  
Gaps: 0

US-09-375-514-22 (1-205) x US-07-936-421-15 (1-36)  
QY 181 LeuAsnArgHisLeuHisThrTrpIleGlnAsp 191  
Db 3 CUGAACGGCACCCUGACACACCGUGGACUCCAGGAU 35

RESULT 2  
US-07-936-421-5  
Sequence 5, Application US/07936421  
Patent No. 5750390  
GENERAL INFORMATION:  
APPLICANT: James D. Thompson  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
BY EXPRESSION OF THE BCL-2  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/936,421  
FILING DATE: 19920826  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

none

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/936,421  
FILING DATE: 19920826  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 197/243  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-936-421-5

Alignment Scores:  
Pred. No.: 164 Length: 33  
Score: 57.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.16% Indels: 0  
Gaps: 0

US-09-375-514-22 (1-205) x US-07-936-421-5 (1-33)  
QY 46 ProGlyIlePheSerGlnProGlyHis 55  
Db 3 CCGGCAUCUCCUCCUCCAGCCGCGGCAC 32

RESULT 3  
US-08-798-897-8/c  
Sequence 8, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cdna

none

US-08-798-897-8

## Alignment Scores:

Pred. No.: 160 Length: 24  
Score: 55.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.98% Indels: 0  
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-798-897-8 (1-24)

QY 188 TptleGlnAspAsnGlyGlyTrp 195

Db 24 TGGATHCARGAYAAAYGGNGNTGG 1

## RESULT 4

US-08-978-523-8/c

Sequence 8, Application US/08978523

Patent No. 5883229

## GENERAL INFORMATION:

APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
OPERATING SYSTEM: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith

## CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/798,897

FILING DATE: February 11, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1483.0140002

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

US-08-978-523-8

## Alignment Scores:

Pred. No.: 160 Length: 24  
Score: 55.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.98% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-978-523-8 (1-24)

QY 188 TptleGlnAspAsnGlyGlyTrp 195

|||||

Db 24 TGGATHCARGAYAAAYGGNGNTGG 1

## RESULT 5

US-08-217-082A-4

Sequence 4, Application US/08217082A

Patent No. 5734033

## GENERAL INFORMATION:

APPLICANT: Reed, John  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE  
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 224 Airport Parkway  
CITY: San Jose  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 95110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/217,082A  
FILING DATE: 24-MAR-1994  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

## APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

## ATTORNEY/AGENT INFORMATION:

NAME: Portney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-08-217-082A-4

## Alignment Scores:

Pred. No.: 1.28e+03 Length: 33  
Score: 47.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.26% Indels: 0  
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-217-082A-4 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200

Db 10 GGAGCTGGGTAGGTGCATCTGGT 33

## RESULT 6

US-08-465-485A-4

Sequence 4, Application US/08465485A

Patent No. 5831066

## GENERAL INFORMATION:

APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29

us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-4
Alignment Scores:
Pred. No.: 1.28e+03 Length: 33
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
Gaps: 0
DB:
US-09-375-514-22 (1-205) x US-08-465-485A-4 (1-33)
QY 193 GlyGlyTrpValGlyAlaSerGly 200
Db 10 GGAGGCTGGGTAGGTGCATCTGGT 33
RESULT 7
US-09-080-285-4
; Sequence 4, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE: 05-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-4
Alignment Scores:
Pred. No.: 1.28e+03 Length: 33
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
Gaps: 0
DB:
US-09-375-514-22 (1-205) x US-09-080-285-4 (1-33)
QY 193 GlyGlyTrpValGlyAlaSerGly 200
Db 10 GGAGGCTGGGTAGGTGCATCTGGT 33
RESULT 8
US-09-724-426-4
; Sequence 4, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-4
Alignment Scores:
Pred. No.: 1.28e+03 Length: 33
Score: 47.00 Matches: 8
;

```

Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 4.26%      Indels: 0  
DB: 4      Gaps: 0

US-09-375-514-22 (1-205) x US-09-724-426-4 (1-33)

QY 193 GlycylTrpValGlyAlaSerGly 200  
Db 10 GGAGGCTGGTAGTGCATCTGCT 33

## RESULT 9

US-07-936-421-8  
; Sequence 8, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/936,421  
; FILING DATE: 19920826  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 197/243  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear

none

## US-07-936-421-8

Alignment Scores:  
Pred. No.: 1.55e+03      Length: 28  
Score: 45.00      Matches: 9  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 4.08%      Indels: 0  
DB: 1      Gaps: 0

US-09-375-514-22 (1-205) x US-07-936-421-8 (1-28)

QY 91 ProValHisLeuAlaLeuArgGln 99  
Db 1 CCUGUGGUCACCUGCCUCCGCCAA 27

## RESULT 10

US-08-480-994-11/c  
; Sequence 11, Application US/08480994  
; Patent No. 5834248  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,994  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-480-994-11

## Alignment Scores:

Pred. No.: 1.54e+03      Length: 24  
Score: 44.00      Matches: 7  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 3.99%      Indels: 0  
DB: 2      Gaps: 0

US-09-375-514-22 (1-205) x US-08-480-994-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGGAGG 3

## RESULT 11

US-08-616-844-11/c  
; Sequence 11, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54

us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

;  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 10036-2711  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/599,654  
 ; FILING DATE: 09-FEB-1996  
 ; CLASSIFICATION: 800  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/485,573  
 ; FILING DATE: 07-JUN-1995  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/386,844  
 ; FILING DATE: 10-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CORUZZI, LAURA A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-041  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ;  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 24 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "synthetic oligonucleotide"  
 ;  
 ; HYPOTHETICAL: NO  
 ;  
 ; US-08-599-654-11  
 ;  
 ; Alignment Scores:  
 ; Pred. No.: 1.54e+03  
 ; Score: 44.00  
 ; Percent Similarity: 100.00%  
 ; Best Local Similarity: 100.00%  
 ; Query Match: 3.99%  
 ; DB: 2  
 ;  
 ; US-09-375-514-22 (1-205) x US-08-599-654-11 (1-24)  
 ;  
 ; QY 140 AspGlyValAsnTrpGlyArg 146  
 ; |||||  
 ; Db 23 GATGGGTGAAGTGGGGGAGG 3  
 ;  
 ; RESULT 13  
 ; US-08-485-573-11/c  
 ; Sequence 11, Application US/08485573  
 ; Patent No. 5968770  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FALB, DEAN A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 ;  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 10036-2711  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/485,573  
 ; FILING DATE: 07-JUN-1995  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/386,844  
 ; FILING DATE: 10-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CORUZZI, LAURA A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-041  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ;  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 24 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "synthetic oligonucleotide"  
 ;  
 ; HYPOTHETICAL: NO  
 ;  
 ; US-08-516-844-11

;  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ;  
 ; ZIP: 10036-2711  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/616,844  
 ; FILING DATE: 15-MAR-1996  
 ; CLASSIFICATION: 800  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/599,654  
 ; FILING DATE: 09-FEB-1996  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/485,573  
 ; FILING DATE: 07-JUN-1995  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/386,844  
 ; FILING DATE: 10-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CORUZZI, LAURA A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-053  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ;  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 24 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "synthetic oligonucleotide"  
 ;  
 ; HYPOTHETICAL: NO  
 ;  
 ; US-08-616-844-11  
 ;  
 ; Alignment Scores:  
 ; Pred. No.: 1.54e+03  
 ; Score: 44.00  
 ; Percent Similarity: 100.00%  
 ; Best Local Similarity: 100.00%  
 ; Query Match: 3.99%  
 ; DB: 2  
 ;  
 ; US-09-375-514-22 (1-205) x US-08-616-844-11 (1-24)  
 ;  
 ; QY 140 AspGlyValAsnTrpGlyArg 146  
 ; |||||  
 ; Db 23 GATGGGTGAAGTGGGGGAGG 3  
 ;  
 ; RESULT 12  
 ; US-08-599-654-11/c  
 ; Sequence 11, Application US/08599654  
 ; Patent No. 5882925  
 ;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FALB, DEAN A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 ;  
 ; NUMBER OF SEQUENCES: 54  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA

CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-485-573-11

Alignment Scores:  
Pred. No.: 1.54e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-485-573-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
|||||  
DB 23 GATGGGTGAACGTGGGGAGG 3

## RESULT 14

US-08-944-868A-11/c  
Sequence 11, Application US/08944868A  
Patent No. 6018025  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,868A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,654  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-944-868A-11

Alignment Scores:  
Pred. No.: 1.54e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-944-868A-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
|||||  
DB 23 GATGGGTGAACGTGGGGAGG 3

## RESULT 15

US-08-944-423A-11/c  
Sequence 11, Application US/08944423A  
Patent No. 6020463  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,423A  
FILING DATE: 06-OCT-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: JUN-07-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-944-423A-11

Alignment Scores:  
Pred. No.: 1.54e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-944-423A-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
DB 23 GATGGGTGAACGGGGGAGG 3

RESULT 16

US-08-925-743-11/c  
Sequence 11, Application US/08925743  
Patent No. 6054558

GENERAL INFORMATION:

APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/925,743

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/485,573

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-032

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

US-08-925-743-11

Alignment Scores:

Pred. No.: 1.54e+03 Length: 24

Score: 44.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.99% Indels: 0

DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-925-743-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
DB 23 GATGGGTGAACGGGGGAGG 3

RESULT 17

US-08-944-496-11/c  
Sequence 11, Application US/08944496  
Patent No. 6124433

GENERAL INFORMATION:

APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/944,496

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/599,654

FILING DATE: 09-FEB-1996

PRIOR APPLICATION NUMBER: US 08/485,573

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/386,844

FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: CORUZZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-104

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic oligonucleotide"

HYPOTHETICAL: NO

US-08-944-496-11

Alignment Scores:

Pred. No.: 1.54e+03 Length: 24

Score: 44.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.99% Indels: 0

DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-944-496-11 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146  
DB 23 GATGGGTGAACGGGGGAGG 3

Db 23 GATCGGGTGAACGGGGAGG 3

RESULT 18  
US-08-925-767-11/c  
Sequence 11, Application US/08925767  
Patent No. 6225084  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/925,767  
FILING DATE: 09-SEPT-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-097  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-925-767-11

Alignment Scores:  
Pred. No.: 1.54e+03 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-08-925-767-11 (1-24)

Qy 140 aspGlyvalAsnTrpGlyArg 146  
Db 23 GATCGGGTGAACGGGGAGG 3

RESULT 19  
US-08-859-998-596/c  
Sequence 596, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG 1

RESULT 20  
US-09-225-928-596/c  
Sequence 596, Application US/09225928  
Patent No. 6352829  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
ADDRESSEE: Jokhadze, George  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:

US-08-859-998-596

Alignment Scores:  
Pred. No.: 2.45e+03 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-859-998-596 (1-25)

Qy 189 ileGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCACGGGTGGGTG



MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 596:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 596:  
US-09-225-928-596

Alignment Scores: Length: 25  
Pred. No.: 2.45e+03  
Score: 42.00  
Percent Similarity: 87.50%  
Best Local Similarity: 87.50%  
Query Match: 3.80%  
Indels: 0  
Gaps: 0  
DB:

US-09-375-514-22 (1-205) x US-09-225-928-596 (1-25)

Qy 189 IleGlnAspAnGlyGlyTrpVal 196  
||||||| |||||||||  
Db 24 ATCCAAGACGAGGTGGTGGTG 1

RESULT 21  
US-08-440-391-21  
; Sequence 21, Application US/08440391  
; Patent No. 5656725  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-908-597A-21  
Alignment Scores: Length: 39  
Pred. No.: 4.52e+03  
Score: 42.00  
Percent Similarity: 87.50%  
Best Local Similarity: 87.50%  
Query Match: 3.80%  
Indels: 0  
Gaps: 0  
DB:

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-440-391-21

Alignment Scores: Length: 39  
Pred. No.: 4.52e+03  
Score: 42.00  
Percent Similarity: 87.50%  
Best Local Similarity: 87.50%  
Query Match: 3.80%  
Indels: 0  
Gaps: 0  
DB:

US-09-375-514-22 (1-205) x US-08-440-391-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112  
||||||| :|||||||  
Db 1 GGGACGACATCAACCGACGCTATGACTCAGAGTTC 36

RESULT 22  
US-08-908-597A-21  
; Sequence 21, Application US/08908597A  
; Patent No. 5863795  
; GENERAL INFORMATION:  
; APPLICANT: CHITTENDEN, Thomas D.; and  
; APPLICANT: LUTZ, Robert J.  
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
; TITLE OF INVENTION: MODULATE APOPTOSIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/908,597A  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,391  
; FILING DATE: 12-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, HENRY N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.147  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-942-8400  
; TELEFAX: 202-942-8484  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-908-597A-21  
Alignment Scores: Length: 39  
Pred. No.: 4.52e+03  
Score: 42.00  
Percent Similarity: 87.50%  
Best Local Similarity: 87.50%  
Query Match: 3.80%  
Indels: 0  
Gaps: 0  
DB:

Percent Similarity: 75.00% Conservative: 2  
Best Local Similarity: 58.33% Mismatches: 3  
Query Match: 3.80% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-908-597A-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112  
||||| :||||| :|||  
Db 1 GGGAGCAGCATCAACCGCGCTATGACTCAGAGTTC 36

## RESULT 23

US-09-236-385A-21

; Sequence 21, Application US/09236385A

; Patent No. 6221615

; GENERAL INFORMATION:

; APPLICANT: CHITTENDEN, Thomas D.; and

; LUTZ, Robert J.

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

; MODULATE APOPTOSIS

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/236,385A

; Filing DATE: 25-Jan-1999

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: WIXON, HENRY N.

; REGISTRATION NUMBER: 32,073

; TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

; TELEPHONE: 202-942-8400

; TELEFAX: 202-942-8400

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-236-385A-21

; Alignment Scores:

Pred. No.: 4.52e+03 Length: 39

Score: 42.00 Matches: 7

Percent Similarity: 75.00% Conservative: 2

Best Local Similarity: 58.33% Mismatches: 3

Query Match: 3.80% Indels: 0

DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-236-385A-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112  
||||| :||||| :|||  
Db 1 GGGAGCAGCATCAACCGCGCTATGACTCAGAGTTC 36

## RESULT 24

PCT-US96-06122-21

; Sequence 21, Application PC/TUS9606122

; GENERAL INFORMATION:

; APPLICANT: IMMUNOGEN, INC.

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS

; TITLE OF INVENTION: WHICH MODULATE APOPTOSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/06122

; Filing DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/440,391

; Filing DATE: 12-MAY-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WIXON, HENRY N.

; REGISTRATION NUMBER: 32,073

; REFERENCE/DOCKET NUMBER: 104322.147PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-942-8400

; TELEFAX: 202-942-8484

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; PCT-US96-06122-21

; Alignment Scores:

Pred. No.: 4.52e+03 Length: 39

Score: 42.00 Matches: 7

Percent Similarity: 75.00% Conservative: 2

Best Local Similarity: 58.33% Mismatches: 3

Query Match: 3.80% Indels: 0

DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US96-06122-21 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112

||||| :||||| :|||

Db 1 GGGAGCAGCATCAACCGCGCTATGACTCAGAGTTC 36

RESULT 25

US-08-426-819A-28

; Sequence 28, Application US/08426819A

; Patent No. 5723318

; GENERAL INFORMATION:

; APPLICANT: Yamaguchi, No. 5723318oml

; APPLICANT: Kojima, Tetsuo

; APPLICANT: Oh-Eda, Masayoshi

; APPLICANT: Hattori, Kunihiro

; TITLE OF INVENTION: Genes Coding for Megakaryocyte

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Birch, Stewart, Kolasch & Birch

; STREET: P.O. Box 747

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,819A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 230-107P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic primer, 850GS"
;
; S-08-426-819A-28
;
; Alignment Scores:
; Pred. No.: 4.41e+03 Length: 33
; Score: 41.00 Matches: 8
; Percent Similarity: 80.00% Conservative: 0
; Best Local Similarity: 80.00% Mismatches: 2
; Query Match: 3.71% Indels: 0
; DB: 1 Gaps: 0
;
; US-09-375-514-22 (1-205) x US-08-426-819A-28 (1-33)
;
; QY 76 AlaAlaProGlyAlaAlaGlyProAla 85
; Db 3 GCGGGCGTGTGCTGGCCAGCC 32
;
; RESULT 26
; US-08-427-097-6/c
; Sequence 6, Application US/08427097
; Patent No. 5668294
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/427,097
; FILING DATE: 21-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: NO
; US-08-878-957-6
;
; Alignment Scores:
; Pred. No.: 4.97e+03 Length: 36
; Score: 41.00 Matches: 8
; Percent Similarity: 88.89% Conservative: 0
; Best Local Similarity: 88.89% Mismatches: 1
; Query Match: 3.71% Indels: 0
; DB: 1 Gaps: 0
;
; US-09-375-514-22 (1-205) x US-08-427-097-6 (1-36)
;
; QY 75 ProAlaAlaProGlyAlaAlaGly 83
; Db 35 CCTGCTGGCGGCTGAGGCTGCAGGA 9
;
; RESULT 27
; US-08-878-957-6/c
; Sequence 6, Application US/08878957
; Patent No. 5965796
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Summers, Anne O.
; APPLICANT: Rugh, Clayton L.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,957
; FILING DATE: 19-JUN-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/427,097
; FILING DATE: 21-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHETICAL: NO
; US-08-878-957-6
;
; Alignment Scores:
; Pred. No.: 4.97e+03 Length: 36
```

Score: 41.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 3.71% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-878-957-6 (1-36)

QY 75 ProAlaProGlyAlaAlaAlaGly 83  
Db 35 CCTGCTGCGCGGTGAGCTGCAGGA 9

## RESULT 28

US-08-145-704-2/c  
; Sequence 2, Application US/08145704  
; Patent No. 5567604  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennewald, Susan  
; APPLICANT: Zendequi, Joseph G.  
; APPLICANT: Joshua O. Ojwang  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/145,704  
; FILING DATE: 28-OCT-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,027  
; FILING DATE: 23-APR-1993  
; NAME: Paul, Thomas D.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5574-CIP  
; TELEPHONE: 713/651-5151  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-145-704-2

Alignment Scores:  
Pred. No.: 5.36e+03 Length: 38  
Score: 41.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 3.71% Indels: 0  
DB: 2 Gaps: 0

US-09-375-514-22 (1-205) x US-08-145-704-2 (1-38)

QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59  
Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3

RESULT 29  
US-08-987-574-2/c  
; Sequence 2, Application US/08987574  
; Patent No. 6150339  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennewald, Susan  
; APPLICANT: Zendequi, Joseph G.  
; APPLICANT: Ojwang, Joshua O.  
; APPLICANT: Hogan, Michael E.  
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
; TITLE OF INVENTION: Oligonucleotides  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/987,574  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04529  
; FILING DATE: 28-OCT-1993  
; APPLICATION NUMBER: US 08/053,027  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5574-CIP  
; TELEPHONE: 713/651-5151  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-987-574-2

Alignment Scores:  
Pred. No.: 5.36e+03 Length: 38  
Score: 41.00 Matches: 8  
Percent Similarity: 50.00% Conservative: 0  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 3.71% Indels: 6  
DB: 3 Gaps: 1

US-09-375-514-22 (1-205) x US-08-987-574-2 (1-38)

QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59  
Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3

## RESULT 30

US-08-535-168-2/c  
; Sequence 2, Application US/08535168  
; Patent No. 6184369  
; GENERAL INFORMATION:  
; APPLICANT: Rando, Robert F.  
; APPLICANT: Fennewald, Susan

Sun Jun 1 14:56:01 2003

us-09-375-514-22.rni

APPLICANT: Zendequi, Joseph G.  
 APPLICANT: Ojwang, Joshua O.  
 APPLICANT: Hogan, Michael E.  
 TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
 TITLE OF INVENTION: Oligonucleotides  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fulbright & Jaworski  
 STREET: 1301 McKinney, Suite 5100  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: U.S.A.  
 ZIP: 77010-3095  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/535,168  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/04529  
 FILING DATE: 28-OCT-1993  
 APPLICATION NUMBER: US 08/053,027  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul, Thomas D.  
 REGISTRATION NUMBER: 32,714  
 REFERENCE/DOCKET NUMBER: D-5574-CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713/651-5151  
 TELEFAX: 713/651-5246  
 TELEX: 762829  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 38 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-535-168-2

Alignment Scores: 5.36e+03 Length: 38  
 Pred. No.: 41.00 Matches: 8  
 Score: 50.00% Conservative: 0  
 Percent Similarity: 50.00% Mismatches: 2  
 Best Local Similarity: 50.00% Indels: 6  
 Query Match: 3.71% Gaps: 1  
 DB:  
 US-09-375-514-22 (1-205) x US-08-535-168-2 (1-38)  
 QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59  
 Db 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3  
 RESULT 31  
 US-09-017-974-2/c  
 ; Sequence 2, Application US/09017974  
 ; Patent No. 6288042  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rando, Robert F.  
 ; APPLICANT: Ojwang, Joshua O.  
 ; APPLICANT: Hogan, Michael E.  
 ; APPLICANT: Wallace, Thomas L.  
 ; APPLICANT: Cossum, Paul A.  
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
 ; TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1800  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: U.S.A.  
 ZIP: 77002-2912  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MS Word 97 (saved as .txt file)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/017,974  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/037,374  
 FILING DATE: 04-FEB-97  
 APPLICATION NUMBER:  
 FILING DATE: 09-DEC-97  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McDaniel, C. Steven  
 REGISTRATION NUMBER: 33,962  
 REFERENCE/DOCKET NUMBER: 1472-06223  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713/238-8010  
 TELEFAX: 713/238-8008  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 38 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-017-974-2  
 Alignment Scores: 5.36e+03 Length: 38  
 Pred. No.: 41.00 Matches: 8  
 Score: 50.00% Conservative: 0  
 Percent Similarity: 50.00% Mismatches: 2  
 Best Local Similarity: 50.00% Indels: 6  
 Query Match: 3.71% Gaps: 1  
 DB:  
 US-09-375-514-22 (1-205) x US-09-017-974-2 (1-38)  
 QY 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59  
 Db 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3  
 RESULT 32  
 US-08-682-255A-2/c  
 ; Sequence 2, Application US/08682255A  
 ; Patent No. 6323185  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rando, Robert F.  
 ; APPLICANT: Fennwald, Susan  
 ; APPLICANT: Zendequi, Joseph G.  
 ; APPLICANT: Ojwang, Joshua O.  
 ; APPLICANT: Hogan, Michael E.  
 ; APPLICANT: Pommier, Yves  
 ; APPLICANT: Mazumder, Abhijit  
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
 ; TITLE OF INVENTION: Oligonucleotides  
 ; NUMBER OF SEQUENCES: 87  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.  
 ; STREET: 600 Travis, Suite 1850  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: U.S.A.  
 ; ZIP: 77002-2912  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-682-255A-2

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 4 Gaps: 1

US-09-375-514-22 (1-205) x US-08-682-255A-2 (1-38)
QY 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59
DB 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
RESULT 33
US-09-429-130-2/c
; Sequence 2, Application US/09429130
; Patent No. 6355785
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; Fennewald, Susan
; Zendegeul, Joseph G.
; Ojwang, Joshua O.
; Hogan, Michael E.
; Pommier, Yves
; Mazumder, Abhijit
; 60/015,714
; TITLE OF INVENTION: Anti-viral Guanosine-Rich
; Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912

```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/429,130
; FILING DATE: 28-Oct-1999
; CLASSIFICATION: <Unknown>
; 19-JULY-95
; 25-MARCH-96
; 19-MARCH-96
; 17-APRIL-96
; 23-APRIL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/682,255
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-429-130-2

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservative: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 4 Gaps: 1

US-09-375-514-22 (1-205) x US-09-429-130-2 (1-38)
QY 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59
DB 32 CCCACCCCA-----CCCCCCCCACCCACACCCC 3
RESULT 34
PCT-US92-09202-10/c
; Sequence 10, Application PC/TUS9209202
; GENERAL INFORMATION:
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Triplex Forming Oligonucleotide Reagents Targeted
; TO THE NEU ONCOGENE PROMOTER AND METHOD OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

Sun Jun 1 14:56:01 2003

us-09-375-514-22.rni

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09202
; FILING DATE: 19921028
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; MOLECULE TYPE: triplex forming oligonucleotide
; HYPOTHETICAL: YES
; PCT-US92-09202-10

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservatives: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US92-09202-10 (1-38)
Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCA-----CCCCCCCCACACCCACACCC 3

RESULT 35
PCT-US93-08329-11/c
; Sequence 11, Application PC/TUS9308329
; GENERAL INFORMATION:
; APPLICANT: Tsai, Ming-Jer
; APPLICANT: Hogan, Michael H
; APPLICANT: O'Malley, Bert W
; APPLICANT: Ing, Nancy H
; TITLE OF INVENTION: Novel Triplex Forming Oligonucleotides
; TITLE OF INVENTION: and Methods for their use
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski Patent Department
; STREET: 1301 McKinney #5100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08329
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US93-08329-11

Alignment Scores:
Pred. No.: 5.36e+03 Length: 38
Score: 41.00 Matches: 8
Percent Similarity: 50.00% Conservatives: 0
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 3.71% Indels: 6
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US93-08329-11 (1-38)
Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59
Db 32 CCCACCCA-----CCCCCCCCACACCCACACCC 3

RESULT 36
PCT-US96-11786-2/c
; Sequence 2, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendegei, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazunder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

MOLECULE TYPE: DNA (genomic)  
PCT-US96-11786-2

Alignment Scores:  
Pred. No.: 5.36e+03 Length: 38  
Score: 41.00 Matches: 8  
Percent Similarity: 50.00% Conservative: 0  
Best Local Similarity: 50.00% Mismatches: 2  
Query Match: 3.71% Indels: 6  
DB: 5 Gaps: 1

US-09-375-514-22 (1-205) x PCT-US96-11786-2 (1-38)

Oy 44 ProAlaProGlyIlePheSerGlnProGlyHsThrProHisPro 59  
Db 32 CCCACCCCA-----CCCCCAGCACACCCACCCC 3

## RESULT 37

PCT-US95-06987-10/c

Sequence 10, Application PC/TUS9506987

GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
TITLE OF INVENTION: The Inhibition of Cytokine Production by  
TITLE OF INVENTION: Oligonucleotides and Inhibition of Tumors Which are  
TITLE OF INVENTION: Responsive to Cytokine Factors  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: US

ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06987  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5669  
TELEPHONE: 713/651-5151  
TELEFAX: 713/651-5246  
TELEX: 762829

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
PCT-US95-06987-10

Alignment Scores:

Pred. No.: 4.11e+03 Length: 27  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US95-06987-10 (1-27)

Oy 53 ProGlyHsThrProHisPro 59

Db 21 CCCACACACACACCCACCCA 1

## RESULT 38

US-08-497-312-8  
Sequence 8, Application US/08497312  
Patent No. 5712120

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified

TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

TITLE OF INVENTION: antibody variable domains, compositions containing them.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

STREET: 215 Y 15, ATABEY PLAYA

CITY: HAVANA

STATE:

COUNTRY: CUBA

ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,312

FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.

REGISTRATION NUMBER: 30,549

REFERENCE/DOCKET NUMBER: 2629US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

TELEX: 388961 1PM04UT

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-08-497-312-8

Alignment Scores:

Pred. No.: 5.87e+03 Length: 35  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 1 Gaps: 0

US-09-375-514-22 (1-205) x US-08-497-312-8 (1-35)

Oy 45 AlaProGlyIlePheSerGlnProGly 54

Db 4 GCCCCAGGCTTCTTCACITTCAGCCCCAGGC 33

## RESULT 39

US-08-497-312-10/c

Sequence 10, Application US/08497312

Patent No. 5712120

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified

TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

TITLE OF INVENTION: antibody variable domains, compositions containing them.

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR



STREET: 215 Y 15, ATABEY PLAYA  
CITY: HAVANA  
STATE:  
COUNTRY: CUBA  
ZIP: 11600  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA: US/08/497,312  
APPLICATION NUMBER: US/08/497,312  
FILING DATE: 30-JUN-1995  
PRIORITY APPLICATION DATA:  
FILING DATE: 30-JUN-1994  
APPLICATION NUMBER: CU 80/94  
ATTORNEY/AGENT INFORMATION:  
NAME: BOND, LAURENCE B.  
REGISTRATION NUMBER: 30,549  
REFERENCE/DOCKET NUMBER: 262905  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 1PM04UT  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-08-497-312-10  
Alignment Scores:  
Pred. No.: 6.11e+03 Length: 36  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 1 Gaps: 0  
US-09-375-514-22 (1-205) x US-08-497-312-10 (1-36)  
Qy 45 AlaProGlyIlePheSerSerGlnProGly 54  
|||||  
Db 32 GCCCAGGCTTCTTCACTTCAGCCCCAGGC 3  
RESULT 40  
US-08-463-682-7  
Sequence 7, Application US/08463682  
Patent No. 6008193  
GENERAL INFORMATION:  
APPLICANT: Leonard Garfinkel, et al.  
TITLE OF INVENTION: Cloning and Production of Human Von  
Willebrand Factor GPIB Binding Domain Polypeptides and  
Methods of Using Same  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,682  
FILING DATE: 05-JUN-1995

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 36537-B2-Y  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-463-682-7  
Alignment Scores:  
Pred. No.: 7.06e+03 Length: 40  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 3 Gaps: 0  
US-09-375-514-22 (1-205) x US-08-463-682-7 (1-40)  
Qy 53 ProGlyHisThrProHisPro 59  
|||||  
Db 1 CCAGGACGAGGCCACATCCA 21  
RESULT 41  
US-08-469-318-110/c  
Sequence 110, Application US/08469318  
Patent No. 6022535  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 196  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,318  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/446,872  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
US-08-469-318-110  
Alignment Scores:  
Pred. No.: 8.67e+03 Length: 40  
Score: 39.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 3.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-375-514-22 (1-205) x US-08-469-318-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91  
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

## RESULT 42

US-08-468-609A-110/C  
; Sequence 110, Application US/08468609A  
; Patent No. 6030812  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.  
; APPLICANT: Bauer, S. C.  
; APPLICANT: Braford-Goldberg, Sarah R.  
; APPLICANT: Caparon, Mair H.  
; APPLICANT: Easton, Alan M.  
; APPLICANT: Klein, Barbara K.  
; APPLICANT: McKearn, John P.  
; APPLICANT: Olins, Peter O.  
; APPLICANT: Paik, Kuman  
; APPLICANT: Thomas, John W.  
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
; ADDRESSEE: Corporate Patent Dept.,  
; STREET: P. O. Box 5110  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60680  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468.609A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/192.325  
; FILING DATE: 14-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bennett, Dennis A.  
; REGISTRATION NUMBER: 34,547  
; REFERENCE/DOCKET NUMBER: C-2790/3  
; TELEPHONE: (314)737-6986  
; TELEFAX: (314)737-6972  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-08-468-609A-110

Alignment Scores:  
Pred. No.: 8.67e+03 Length: 40  
Score: 39.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 3.53% Indels: 0  
DB: 3 Gaps: 0

US-09-375-514-22 (1-205) x US-08-468-609A-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91  
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

## RESULT 43

US-08-446-872A-110/C  
; Sequence 110, Application US/08446872A  
; Patent No. 6361977  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.  
; APPLICANT: Bauer, S. C.  
; APPLICANT: Braford-Goldberg, Sarah R.  
; APPLICANT: Caparon, Mair H.  
; APPLICANT: Easton, Alan M.  
; APPLICANT: Klein, Barbara K.  
; APPLICANT: McKearn, John P.  
; APPLICANT: Olins, Peter O.  
; APPLICANT: Paik, Kuman  
; APPLICANT: Thomas, John W.  
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
; ADDRESSEE: Corporate Patent Dept.,  
; STREET: P. O. Box 5110  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60680  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446.872A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/192.325  
; FILING DATE: 14-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bennett, Dennis A.  
; REGISTRATION NUMBER: 34,547  
; REFERENCE/DOCKET NUMBER: C-2790/1  
; TELEPHONE: (314)737-6986  
; TELEFAX: (314)737-6972  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-08-446-872A-110

Alignment Scores:  
Pred. No.: 8.67e+03 Length: 40  
Score: 39.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 3.53% Indels: 0  
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-08-446-872A-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91  
DB 38 CCTGCCATGGCTCCAGTACCACCA 15

## RESULT 44

US-08-762-227A-110/C  
; Sequence 110, Application US/08762227A  
; Patent No. 6436387

GENERAL INFORMATION:  
APPLICANT: Adams, Mark A.  
Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Mairé H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olines, Peter O.  
Paik, Kuman  
Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion Protein  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dennis A. Bennett, G.D. Searle & Co.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,227A  
FILING DATE: 09-Dec-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-08-762-227A-110

Alignment Scores: Length: 40  
Pred. No.: 8.67e+03  
Score: 39.00  
Percent Similarity: 100.00%  
Best Local Similarity: 75.00%  
Query Match: 3.53%  
DB: 4

US-09-375-514-22 (1-205) x US-08-762-227A-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91  
Db 38 CCTGCATGGCTCCAGTACCACCA 15

RESULT 45  
PCT-US95-01185-110/c  
Sequence 110, Application PC/TUS9501185  
GENERAL INFORMATION:  
APPLICANT: Adams, Mark A.  
Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Mairé H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olines, Peter O.  
Paik, Kuman  
Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion Protein  
NUMBER OF SEQUENCES: 196  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dennis A. Bennett, G.D. Searle & Co.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01185  
FILING DATE: 02-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-09-375-514-22 (1-205) x PCT-US95-01185-110 (1-40)

QY 84 ProAlaLeuSerProValProPro 91  
Db 38 CCTGCATGGCTCCAGTACCACCA 15

RESULT 46  
US-09-485-636-2/c  
Sequence 2, Application US/09485636  
Patent No. 6316196  
GENERAL INFORMATION:  
APPLICANT: John Edward No. 6316196ris MORTEN  
TITLE OF INVENTION: METHODS FOR ANALYZING LTC4 SYNTHASE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/485,636  
FILING DATE: 15-Feb-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/02468  
FILING DATE: August 18, 1998  
APPLICATION NUMBER: GB 9717766.1  
FILING DATE: August 22, 1997  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid

```
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-485-636-2

Alignment Scores:
Pred. No.: 7.17e+03 Length: 30
Score: 38.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-485-636-2 (1-30)

QY 38 AlaProGlyAlaAlaProAla 45
|||||
DB 29 GCCCGCGCTGGAGCGCCCGGCC 6

RESULT 47
PCT-US95-06987-3
; Sequence 3, Application PC/TUS9506987
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; TITLE OF INVENTION: The Inhibition of Cytokine Production by
; TITLE OF INVENTION: Oligonucleotides and Inhibition of Tumors which are
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US95/06987
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5669
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06987-3

Alignment Scores:
Pred. No.: 8.82e+03 Length: 35
Score: 38.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 3.44% Indels: 0
DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US95-06987-3 (1-35)

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-485-636-2

Alignment Scores:
Pred. No.: 7.17e+03 Length: 30
Score: 38.00 Matches: 7
Percent Similarity: 87.50% Conservative: 0
Best Local Similarity: 87.50% Mismatches: 1
Query Match: 3.44% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-485-636-2 (1-30)

QY 38 AlaProGlyAlaAlaProAla 45
|||||
DB 29 GCCCGCGCTGGAGCGCCCGGCC 6

RESULT 47
PCT-US95-06987-3
; Sequence 3, Application PC/TUS9506987
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; TITLE OF INVENTION: The Inhibition of Cytokine Production by
; TITLE OF INVENTION: Oligonucleotides and Inhibition of Tumors which are
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US95/06987
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5669
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06987-3

Alignment Scores:
Pred. No.: 8.82e+03 Length: 35
Score: 38.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 3.44% Indels: 0
DB: 5 Gaps: 0

US-09-375-514-22 (1-205) x PCT-US95-06987-3 (1-35)

QY 55 HistHrProHisProAlaAlaSer 62
|||||
DB 9 CACACTCCCATCTCCTCCTGCTCC 32

RESULT 48
US-09-367-750-5
; Sequence 5, Application US/09367750
; Patent No. 6436639
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Ossina, Natalya K.
; TITLE OF INVENTION: Bak PROMOTER EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LXR BIOTECHNOLOGY INC.
; STREET: 3095 Richmond Parkway, Suite 213
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/367,750
; FILING DATE: 07-DEC-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-14-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-367-750-5

Alignment Scores:
Pred. No.: 9.17e+03 Length: 36
Score: 38.00 Matches: 6
Percent Similarity: 70.00% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 3
Query Match: 3.44% Indels: 0
DB: 4 Gaps: 0

US-09-375-514-22 (1-205) x US-09-367-750-5 (1-36)

QY 135 GluGluLeuPheArgAspGlyValAsnTrp 144
|||||
DB 7 GAATTCCTGTTTGAGAGTGCGCAATTGG 36

RESULT 49
US-08-217-082A-3/C
; Sequence 3, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
```

us-09-375-514-22.rni

Sun Jun 1 14:56:01 2003

```

; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Portney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-3

```

```

Alignment Scores:
Pred. No.: 5,04e+03 Length: 20
Score: 37.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.35% Indels: 0
DB: 2 Gaps: 0

```

```

US-09-375-514-22 (1-205) x US-08-465-485A-3 (1-20)

```

```

Qy 193 GlyGlyTrpValGlyAla 198
Db 20 GGAGGCTGGGTAGGTGCA 3

```

```

Search completed: May 31, 2003, 23:23:16
Job time : 67 secs

```

```

; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Portney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: YES
; US-08-217-082A-3

```

```

Alignment Scores:
Pred. No.: 5,04e+03 Length: 20
Score: 37.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.35% Indels: 0
DB: 1 Gaps: 0

```

```

US-09-375-514-22 (1-205) x US-08-217-082A-3 (1-20)

```

```

Qy 193 GlyGlyTrpValGlyAla 198
Db 20 GGAGGCTGGGTAGGTGCA 3

```

```

RESULT 50
US-08-465-485A-3/c
Sequence 3, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995

```



Sun Jun '1 14:55:59 2003

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 18:42:35 ; Search time 1764 Seconds  
(without alignments)  
3382.129 Million cell updates/sec

US-09-375-514-22

Title: 1104  
Sequence: 1 MAHAGRTGYDREIVMYIH.....HTWIQDNGWVGASGDVSLG 205

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 770742

Minimum DB seq length: 10  
Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Command line parameters: -dev-xlp  
-Q-/cgn2\_1/USPTO.spool/JUS0375514/runat\_28052003\_165345\_18660/app\_query.fasta\_1.391  
-DB-GenEmbl -QFMT-fastap -SUFFIX-rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=500  
-DOCALLIGN=200 -THR\_SCORE=500 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=10 -MAXLEN=40 -ICPU=3  
-USER=US0375514 @CNC1.1.1420 @runat\_28052003\_165345\_18660 -NCPU=6 -LONGLOG  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

- Database :
- 1: gb.ba.\*
  - 2: gb.htg.\*
  - 3: gb.in.\*
  - 4: gb.om.\*
  - 5: gb.ov.\*
  - 6: gb.pat.\*
  - 7: gb.ph.\*
  - 8: gb.pl.\*
  - 9: gb.pr.\*
  - 10: gb.ro.\*
  - 11: gb.sts.\*
  - 12: gb.sy.\*
  - 13: gb.un.\*
  - 14: gb.vl.\*
  - 15: em.ba.\*
  - 16: em.fun.\*
  - 17: em.in.\*
  - 18: em.in.\*
  - 19: em.mu.\*
  - 20: em.mu.\*
  - 21: em.or.\*
  - 22: em.ov.\*
  - 23: em.pat.\*
  - 24: em.ph.\*
  - 25: em.pl.\*
  - 26: em.ro.\*
  - 27: em.sts.\*
  - 28: em.un.\*

- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rnd.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htg\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	71	6.4	39	6	AX377550 Sequence
C 2	71	6.4	39	6	AX377551 Sequence
C 3	66	6.0	36	6	AR007301 Sequence
C 4	63	5.7	39	6	AX377552 Sequence
C 5	57	5.2	33	6	AR007291 Sequence
C 6	55	5.0	24	6	AR020782 Sequence
C 7	47	4.3	33	6	AR052606 Sequence
C 8	47	4.3	33	6	196085 Sequence 4
C 9	45	4.1	28	6	AR007294 Sequence
C 10	45	4.1	36	9	AJ005138 Homo sapi
C 11	44	4.0	24	6	AR053546 Sequence
C 12	44	4.0	24	6	AR065873 Sequence
C 13	44	4.0	24	6	AR080355 Sequence
C 14	44	4.0	24	6	AR148310 Sequence
C 15	43	3.9	28	6	AX031294 Sequence
C 16	43	3.9	28	13	AX031320 Sequence
C 17	42	3.8	25	6	AR090476 Sequence
C 18	42	3.8	25	6	AR197511 Sequence
C 19	42	3.8	39	6	I60569 Sequence 21
C 20	41	3.7	31	6	AX022526 Sequence
C 21	41	3.7	31	6	AX030814 Sequence
C 22	41	3.7	33	6	I89980 Sequence 28
C 23	41	3.7	33	9	S80834 gamma delta
C 24	41	3.7	36	6	I65770 Sequence 6
C 25	41	3.7	38	6	AR168776 Sequence
C 26	41	3.7	38	6	AR200245 Sequence
C 27	41	3.7	38	6	I27770 Sequence 2
C 28	40	3.6	35	6	A47631 Sequence 8
C 29	40	3.6	36	6	I82275 Sequence 10
C 30	40	3.6	36	6	A68670 Sequence 16
C 31	40	3.6	36	6	A68670 Sequence 16
C 32	40	3.6	36	6	I82277 Sequence 10
C 33	40	3.6	40	6	AR096669 Sequence
C 34	40	3.6	40	6	AX262441 Sequence
C 35	39	3.5	31	6	AX248386 Sequence
C 36	39	3.5	35	6	AX097404 Sequence
C 37	39	3.5	40	6	AR202261 Sequence
C 38	39	3.5	31	6	AX080990 Sequence
C 39	38.5	3.5	31	6	AX248293 Sequence
C 40	38	3.4	20	6	AX224988 Sequence
C 41	38	3.4	24	6	AX224989 Sequence
C 42	38	3.4	24	6	AX113808 Sequence 2
C 43	38	3.4	30	6	A98608 Sequence 2
C 44	38	3.4	30	9	S65556 COL1A1-coll
C 45	38	3.4	31	6	AX248864 Sequence
C 46	38	3.4	31	6	AX477731 Sequence
C 47	38	3.4	31	6	AX477732 Sequence 10
C 48	38	3.4	33	6	A36722 Sequence 10
C 49	38	3.4	36	6	AX247606 Sequence
C 50	37	3.4	20	6	AR052605 Sequence

[illegible]



197	33.5	3.0	33	6	A07282	A07282 Synthetic P	33	3.0	30	6	AR067282	Sequence
c 198	33.5	3.0	33	6	AR123470	AR123470 Sequence	33	3.0	30	6	AR073896	Sequence
199	33.5	3.0	36	6	AX014266	AX014266 Sequence	33	3.0	30	6	AR125785	Sequence
c 200	33.5	3.0	39	6	I06515	I06515 Sequence 19	33	3.0	30	6	AX037347	Sequence
c 201	33.5	3.0	40	6	AX168014	AX168014 Sequence	33	3.0	30	6	AX139036	Sequence
c 202	33.5	3.0	40	6	BD000242	BD000242 Cell for	33	3.0	30	6	AX139036	Sequence
203	33	3.0	40	6	AR168822	AR168822 Sequence	33	3.0	30	6	AX317266	Sequence
204	33	3.0	16	6	AR200291	AR200291 Sequence	33	3.0	30	6	E43302	Composition
205	33	3.0	17	6	AR168807	AR168807 Sequence	33	3.0	30	6	I47197	Sequence 12
206	33	3.0	17	6	AR168820	AR168820 Sequence	33	3.0	30	9	S66556	COL1A1-coll
207	33	3.0	17	6	AR168832	AR168832 Sequence	33	3.0	30	9	HUMPLTP21	U37828 Human hosp
208	33	3.0	17	6	AR168833	AR168833 Sequence	33	3.0	31	6	AR028653	Sequence
209	33	3.0	17	6	AR168834	AR168834 Sequence	33	3.0	31	6	AR053746	Sequence
210	33	3.0	17	6	AR168842	AR168842 Sequence	33	3.0	31	6	AR146246	Sequence
211	33	3.0	17	6	AR168846	AR168846 Sequence	33	3.0	31	6	AR178200	Sequence
212	33	3.0	17	6	AR168849	AR168849 Sequence	33	3.0	31	6	AX229083	Sequence
213	33	3.0	17	6	AR168853	AR168853 Sequence	33	3.0	31	6	AX249407	Sequence
214	33	3.0	17	6	AR168861	AR168861 Sequence	33	3.0	31	6	AX280690	Sequence
215	33	3.0	17	6	AR200276	AR200276 Sequence	33	3.0	31	6	AX280691	Sequence
216	33	3.0	17	6	AR200289	AR200289 Sequence	33	3.0	31	6	AX405358	Sequence
217	33	3.0	17	6	AR200301	AR200301 Sequence	33	3.0	31	6	AX405365	Sequence
218	33	3.0	17	6	AR200302	AR200302 Sequence	33	3.0	31	6	I73325	Sequence 21
219	33	3.0	17	6	AR200303	AR200303 Sequence	33	3.0	32	6	AR176509	Sequence
220	33	3.0	17	6	AR200311	AR200311 Sequence	33	3.0	32	6	AX254368	Sequence
221	33	3.0	17	6	AR200315	AR200315 Sequence	33	3.0	32	6	AX254378	Sequence
222	33	3.0	17	6	AR200318	AR200318 Sequence	33	3.0	32	6	AX254378	Sequence
223	33	3.0	17	6	AR200322	AR200322 Sequence	33	3.0	32	6	AX31817	Synthetic P
224	33	3.0	17	6	AR200330	AR200330 Sequence	33	3.0	32	6	AR039150	Sequence
225	33	3.0	17	6	I27801	I27801 Sequence 33	33	3.0	32	6	AR065280	Sequence
226	33	3.0	18	6	AR168777	AR168777 Sequence	33	3.0	32	6	AR176491	Sequence
227	33	3.0	18	6	AR168805	AR168805 Sequence	33	3.0	32	6	AX210344	Sequence
228	33	3.0	18	6	AR168806	AR168806 Sequence	33	3.0	32	6	AX358652	Sequence
229	33	3.0	18	6	AR200246	AR200246 Sequence	33	3.0	32	6	E10386	PCR primer
230	33	3.0	18	6	AR200274	AR200274 Sequence	33	3.0	32	6	I59457	Sequence 4
231	33	3.0	18	6	AR200275	AR200275 Sequence	33	3.0	32	6	AR028418	Sequence
232	33	3.0	18	6	I27771	I27771 Sequence 3	33	3.0	32	6	AR100590	Sequence
233	33	3.0	18	6	I27799	I27799 Sequence 31	33	3.0	32	6	AR130928	Sequence
234	33	3.0	18	6	I27800	I27800 Sequence 32	33	3.0	32	6	AR161894	Sequence
235	33	3.0	18	6	I39711	I39711 Sequence 74	33	3.0	32	6	AX015343	Sequence
c 236	33	3.0	18	6	AR108196	AR108196 Sequence	33	3.0	32	6	AX467534	Sequence
c 237	33	3.0	20	6	AX147401	AX147401 Sequence	33	3.0	32	6	AX467534	Sequence
238	33	3.0	21	6	A46336	A46336 Sequence 7	33	3.0	32	6	AX467534	Sequence
c 239	33	3.0	21	6	A46337	A46337 Sequence 8	33	3.0	32	6	AX467534	Sequence
c 240	33	3.0	21	6	AX342527	AX342527 Sequence	33	3.0	32	6	AX467534	Sequence
c 241	33	3.0	22	6	A41472	A41472 Sequence 4	33	3.0	32	6	AX467534	Sequence
c 242	33	3.0	22	6	AR067587	AR067587 Sequence	33	3.0	32	6	AX467534	Sequence
c 243	33	3.0	22	6	I32323	I32323 Sequence 4	33	3.0	32	6	AX467534	Sequence
244	33	3.0	23	6	I17099	I17099 Sequence 14	33	3.0	32	6	AX467534	Sequence
245	33	3.0	23	6	I63494	I63494 Sequence 14	33	3.0	32	6	AX467534	Sequence
c 246	33	3.0	25	6	AX115704	AX115704 Sequence	33	3.0	32	6	AX467534	Sequence
247	33	3.0	25	6	AX476206	AX476206 Sequence	33	3.0	32	6	AX467534	Sequence
248	33	3.0	25	6	AX476207	AX476207 Sequence	33	3.0	32	6	AX467534	Sequence
249	33	3.0	25	6	AX476209	AX476209 Sequence	33	3.0	32	6	AX467534	Sequence
250	33	3.0	25	6	AX476210	AX476210 Sequence	33	3.0	32	6	AX467534	Sequence
251	33	3.0	26	6	AX119189	AX119189 Sequence	33	3.0	32	6	AX467534	Sequence
252	33	3.0	26	6	AX002479	AX002479 Sequence	33	3.0	32	6	AX467534	Sequence
c 253	33	3.0	26	6	AX146722	AX146722 Sequence	33	3.0	32	6	AX467534	Sequence
254	33	3.0	26	6	I52050	I52050 Sequence 2	33	3.0	32	6	AX467534	Sequence
255	33	3.0	27	6	AR024410	AR024410 Sequence	33	3.0	32	6	AX467534	Sequence
256	33	3.0	27	6	AR091783	AR091783 Sequence	33	3.0	32	6	AX467534	Sequence
257	33	3.0	27	6	AR143832	AR143832 Sequence	33	3.0	32	6	AX467534	Sequence
258	33	3.0	27	6	AR168808	AR168808 Sequence	33	3.0	32	6	AX467534	Sequence
259	33	3.0	27	6	AR200277	AR200277 Sequence	33	3.0	32	6	AX467534	Sequence
c 260	33	3.0	27	6	AX183859	AX183859 Sequence	33	3.0	32	6	AX467534	Sequence
261	33	3.0	27	6	AX469904	AX469904 Sequence	33	3.0	32	6	AX467534	Sequence
262	33	3.0	27	6	AX469912	AX469912 Sequence	33	3.0	32	6	AX467534	Sequence
263	33	3.0	27	6	I27802	I27802 Sequence 34	33	3.0	32	6	AX467534	Sequence
264	33	3.0	27	6	I60572	I60572 Sequence 27	33	3.0	32	6	AX467534	Sequence
265	33	3.0	27	6	I71202	I71202 Sequence 54	33	3.0	32	6	AX467534	Sequence
266	33	3.0	27	6	I83761	I83761 Sequence 54	33	3.0	32	6	AX467534	Sequence
267	33	3.0	28	6	AR173104	AR173104 Sequence	33	3.0	32	6	AX467534	Sequence
268	33	3.0	28	6	AR085809	AR085809 Sequence	33	3.0	32	6	AX467534	Sequence
269	33	3.0	29	6	I07501	I07501 Sequence 1	33	3.0	32	6	AX467534	Sequence

C 343	32	2.9	18	6	AR052624	Sequence	416	32	2.9	28	6	AR099199	Sequence
C 344	32	2.9	18	6	ARI16926	Sequence	417	32	2.9	28	6	AR099219	Sequence
C 345	32	2.9	18	6	ARI40496	Sequence	418	32	2.9	28	6	ARI54293	Sequence
C 346	32	2.9	18	6	ARI46347	Sequence	419	32	2.9	28	6	ARI97123	Sequence
C 347	32	2.9	18	6	ARI46347	Sequence	420	32	2.9	28	6	ARI97415	Sequence
C 348	32	2.9	18	6	ARI54716	Sequence	421	32	2.9	29	6	IO1627	Sequence 4
C 349	32	2.9	18	6	ARI167448	Sequence	422	32	2.9	29	6	IO7502	Sequence 2
C 350	32	2.9	18	6	AX015198	Sequence	423	32	2.9	29	6	S43673	Sequence
C 351	32	2.9	18	6	AX020948	Sequence	424	32	2.9	29	6	S43673	NADH dehydr
C 352	32	2.9	18	6	AX020954	Sequence	425	32	2.9	29	6	AX1495	Nucleotide
C 353	32	2.9	18	6	AX040169	Sequence	426	32	2.9	30	6	AX1499	Nucleotide
C 354	32	2.9	18	6	AX040403	Sequence	427	32	2.9	30	6	AX1501	Nucleotide
C 355	32	2.9	18	6	AX063576	Sequence	428	32	2.9	30	6	AR077134	Sequence
C 356	32	2.9	18	6	AX081353	Sequence	429	32	2.9	30	6	AR087144	Sequence
C 357	32	2.9	18	6	AX083693	Sequence	430	32	2.9	30	6	AR087561	Sequence
C 358	32	2.9	18	6	AX088930	Sequence	431	32	2.9	30	6	AX180867	Sequence
C 359	32	2.9	18	6	AX103809	Sequence	432	32	2.9	30	6	AX180867	Sequence
C 360	32	2.9	18	6	AX103862	Sequence	433	32	2.9	30	6	AX468215	Sequence
C 361	32	2.9	18	6	AX103863	Sequence	434	32	2.9	30	6	ES5287	Novel metal
C 362	32	2.9	18	6	AX103899	Sequence	435	32	2.9	30	6	E64508	Sugar-respo
C 363	32	2.9	18	6	AX105211	Sequence	436	32	2.9	30	6	I23958	Sequence 6
C 364	32	2.9	18	6	AX135635	Sequence	437	32	2.9	30	6	U37809	Human phosph
C 365	32	2.9	18	6	AX278114	Sequence	438	32	2.9	31	6	AX248033	Sequence
C 366	32	2.9	18	6	AX283183	Sequence	439	32	2.9	31	6	AX248033	Sequence
C 367	32	2.9	18	6	AX283250	Sequence	440	32	2.9	31	6	AX248352	Sequence
C 368	32	2.9	18	6	AX355727	Sequence	441	32	2.9	31	6	AX248814	Sequence
C 369	32	2.9	18	6	AX355728	Sequence	442	32	2.9	31	6	BD005987	Sequence
C 370	32	2.9	18	6	AX455638	Sequence	443	32	2.9	31	6	E10701	Primer. 9/1
C 371	32	2.9	18	6	AX468484	Sequence	444	32	2.9	31	6	II16002	Sequence 5
C 372	32	2.9	18	6	BD009103	Immunoti	445	32	2.9	31	6	AR162778	Sequence
C 373	32	2.9	18	6	I96098	Sequence 17	446	32	2.9	32	6	AR182223	Sequence
C 374	32	2.9	19	6	AX083694	Sequence	447	32	2.9	32	6	E06343	Primer. 9/1
C 375	32	2.9	19	6	AX083695	Sequence	448	32	2.9	32	6	E06539	Primer. 9/1
C 376	32	2.9	20	6	AR182888	Sequence	449	32	2.9	32	6	I89977	Sequence 25
C 377	32	2.9	20	6	AX058429	Sequence	450	32	2.9	33	6	A36827	Sequence 46
C 378	32	2.9	20	6	AX058860	Sequence	451	32	2.9	33	6	A45614	Sequence 8
C 379	32	2.9	20	6	AX103895	Sequence	452	32	2.9	33	6	A66582	Sequence 14
C 380	32	2.9	20	6	AX103917	Sequence	453	32	2.9	33	6	AR021437	Sequence
C 381	32	2.9	20	6	AX224980	Sequence	454	32	2.9	33	6	AR033071	Sequence
C 382	32	2.9	20	6	AX224987	Sequence	455	32	2.9	33	6	AR042999	Sequence
C 383	32	2.9	20	6	AX355729	Sequence	456	32	2.9	33	6	AR075905	Sequence
C 384	32	2.9	20	6	AX355738	Sequence	457	32	2.9	33	6	AR075905	Sequence
C 385	32	2.9	21	6	A75769	Sequence 38	458	32	2.9	33	6	AR07694	Sequence
C 386	32	2.9	21	6	AR085105	Sequence	459	32	2.9	33	6	AR147785	Sequence
C 387	32	2.9	21	6	AX278112	Sequence	460	32	2.9	33	6	AR161332	Sequence
C 388	32	2.9	21	6	AX278528	Sequence	461	32	2.9	33	6	AX033433	Sequence
C 389	32	2.9	21	6	AX283524	Sequence	462	32	2.9	33	6	AX033443	Sequence
C 390	32	2.9	22	6	AX031293	Sequence	463	32	2.9	33	6	E10537	PCR primer
C 391	32	2.9	22	6	E33374	NA+-ATPase	464	32	2.9	33	6	I50558	Sequence 12
C 392	32	2.9	22	13	AX031319	Sequence	465	32	2.9	33	6	I62990	Sequence 11
C 393	32	2.9	23	6	AX083687	Sequence	466	32	2.9	33	6	I88743	Sequence 11
C 394	32	2.9	23	6	AX083688	Sequence	467	32	2.9	33	6	U27253	Human isola
C 395	32	2.9	23	6	AX297646	Sequence	468	32	2.9	34	6	X59234	H.sapiens m
C 396	32	2.9	24	6	AX036508	Sequence	469	32	2.9	34	6	X69236	H.sapiens m
C 397	32	2.9	24	6	AX290531	Sequence	470	32	2.9	34	6	A30422	Probe/PCR p
C 398	32	2.9	24	6	AX446906	Sequence	471	32	2.9	34	6	AR045239	Sequence
C 399	32	2.9	24	6	E31769	Novel metap	472	32	2.9	34	6	AR117304	Sequence
C 400	32	2.9	25	6	A99107	Sequence 11	473	32	2.9	34	6	AR117304	Sequence
C 401	32	2.9	25	6	AR175422	Sequence	474	32	2.9	34	6	AX349888	Sequence
C 402	32	2.9	25	6	AX189384	Sequence	475	32	2.9	34	6	AX349888	Sequence
C 403	32	2.9	26	6	AR8675	Sequence 82	476	32	2.9	34	6	AX452070	Sequence
C 404	32	2.9	26	6	A90642	Sequence 82	477	32	2.9	34	6	E06320	Primer. 9/1
C 405	32	2.9	26	6	AX055459	Sequence	478	32	2.9	35	6	E06516	Truncated c
C 406	32	2.9	27	6	AR004426	Sequence	479	32	2.9	35	6	E35109	Sequence 54
C 407	32	2.9	27	6	AR018064	Sequence	480	32	2.9	35	6	I49868	Sequence 32
C 408	32	2.9	27	6	AR018065	Sequence	481	32	2.9	35	6	I52291	Sequence 32
C 409	32	2.9	27	6	AR035303	Sequence	482	32	2.9	35	6	SSREP5	Scilla sibe
C 410	32	2.9	27	6	AX317285	Sequence	483	32	2.9	35	6	AR052604	Sequence
C 411	32	2.9	27	6	AX406816	Sequence	484	32	2.9	35	6	AR052604	Sequence
C 412	32	2.9	27	6	I43661	Sequence 13	485	32	2.9	35	6	AR085273	Sequence
C 413	32	2.9	27	6	I86720	Sequence 8	486	32	2.9	35	6	AX262313	Sequence
C 414	32	2.9	28	6	AR090088	Sequence	487	32	2.9	35	6	AX382281	Sequence
C 415	32	2.9	28	6	AR090380	Sequence	488	32	2.9	36	6	AX382285	Sequence

c 489 32 2.9 36 6 AR069551 Sequence  
c 490 32 2.9 36 6 AR179634 Sequence  
c 491 32 2.9 36 6 AX017162 Sequence  
c 492 32 2.9 36 6 AX357323 Sequence  
c 493 32 2.9 36 6 E08282 Sequence  
c 494 32 2.9 36 6 I92026 Sequence  
c 495 32 2.9 36 6 A31736 Sequence  
c 496 32 2.9 37 6 AR182877 Sequence  
c 497 32 2.9 37 6 AX424976 Sequence  
c 498 32 2.9 37 6 I20696 Sequence  
c 499 32 2.9 37 6 I20717 Sequence  
500 32 2.9 38 6 A23776 Sequence

## ALIGNMENTS

RESULT 1  
AX377550/c 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377550  
DEFINITION Sequence 27 from Patent WO0212553.  
ACCESSION AX377550  
VERSION AX377550.1 GI:19573736  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 27 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39  
BASE COUNT 4 a 8 c 21 g 6 t  
ORIGIN /db\_xref="taxon:9606"

Alignment Scores:  
Pred. No.: 1.57e+03 Length: 39  
Score: 71.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.43% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377550 (1-39)

QY 53 ProGlyHisThrProHisProAlaAlaSerArgAsp 64  
|||||  
39 CCCGGGCACAGCCGCCATCCAGCGCGATCCCGCGAC 4

RESULT 2  
AX377551 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377551  
DEFINITION Sequence 28 from Patent WO0212553.  
ACCESSION AX377551  
VERSION AX377551.1 GI:19573737  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 28 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39

Alignment Scores:  
Pred. No.: 1.57e+03 Length: 39  
Score: 71.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.43% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377551 (1-39)  
QY 53 ProGlyHisThrProHisProAlaAlaSerArgAsp 64  
|||||  
39 CCCGGGCACAGCCGCCATCCAGCGCGATCCCGCGAC 4

BASE COUNT 7 a 21 c 9 g 2 t  
ORIGIN /db\_xref="taxon:9606"

US-09-375-514-22 (1-205) x AX377551 (1-39)

QY 53 ProGlyHisThrProHisProAlaAlaSerArgAsp 64  
|||||  
39 CCCGGGCACAGCCGCCATCCAGCGCGATCCCGCGAC 38

RESULT 3  
AR007301 36 bp DNA linear PAT 04-DEC-1998  
LOCUS AR007301  
DEFINITION Sequence 15 from patent US 5750390.  
ACCESSION AR007301  
VERSION AR007301.1 GI:3966785  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Thompson,J.D. and Draper,K.G.  
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL Patent: US 5750390-A 15 12-MAY-1998;  
FEATURES  
source 1. .36  
BASE COUNT 10 a 13 c 8 g 5 t  
ORIGIN /db\_xref="taxon:9606"

Alignment Scores:  
Pred. No.: 1.57e+03 Length: 39  
Score: 71.00 Matches: 12  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.43% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)  
QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191  
|||||  
3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4  
AX377552 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377552  
DEFINITION Sequence 29 from Patent WO0212553.  
ACCESSION AX377552  
VERSION AX377552.1 GI:19573738  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39

Alignment Scores:  
Pred. No.: 2.86e+03 Length: 36  
Score: 66.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.98% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)

QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191  
|||||  
3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4  
AX377552 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377552  
DEFINITION Sequence 29 from Patent WO0212553.  
ACCESSION AX377552  
VERSION AX377552.1 GI:19573738  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39

Alignment Scores:  
Pred. No.: 2.86e+03 Length: 36  
Score: 66.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.98% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)

QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191  
|||||  
3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4  
AX377552 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377552  
DEFINITION Sequence 29 from Patent WO0212553.  
ACCESSION AX377552  
VERSION AX377552.1 GI:19573738  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39

Alignment Scores:  
Pred. No.: 2.86e+03 Length: 36  
Score: 66.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.98% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007301 (1-36)

QY 181 LeuAsnArgHisLeuHisThrTriPleGlnAsp 191  
|||||  
3 CTGAACCGGACCTGCACACCTGGATCCAGGAT 35

RESULT 4  
AX377552 39 bp DNA linear PAT 18-MAR-2002  
LOCUS AX377552  
DEFINITION Sequence 29 from Patent WO0212553.  
ACCESSION AX377552  
VERSION AX377552.1 GI:19573738  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrendorf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1. .39

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 7 a 20 c 9 g 3 t
ORIGIN

Alignment Scores:
Pred. No.: 4.61e+03 Length: 39
Score: 63.00 Matches: 11
Percent Similarity: 91.67% Conservative: 0
Best Local Similarity: 91.67% Mismatches: 1
Query Match: 5.71% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX377552 (1-39)

QY 53 ProGlyHisThrProHisProAlaAlaSerArgAsp 64
3 CCGGGCACACGCCCATTCAGCCGCGATCCCGGCAC 38
RESULT 5
AR007291 AR007291 33 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 5 from patent US 5750390.
ACCESSION AR007291
VERSION AR007291.1 GI:3966775
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression
of the bcl-2 gene
JOURNAL Patent: US 5750390-A 5 12-MAY-1998;
FEATURES Location/Qualifiers
source
1..33
BASE COUNT 5 a 16 c 7 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 8.84e+03 Length: 33
Score: 57.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.16% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007291 (1-33)

QY 46 ProGlyIlePheSerSerGlnProGlyHis 55
3 CCGGGCATCTTCTCTCCAGCCGCGGCAC 32
RESULT 6
AR020782/c AR020782 24 bp DNA linear PAT 05-DEC-1998
LOCUS
DEFINITION Sequence 8 from patent US 5789201.
ACCESSION AR020782
VERSION AR020782.1 GI:3975397
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Guastella,J.
TITLE Genes coding for bcl-y a bcl-2 homologue
JOURNAL Patent: US 5789201-A 8 04-AUG-1998;
FEATURES Location/Qualifiers
source
1..24
BASE COUNT 3 a 9 c 1 g 5 t 6 others
ORIGIN

/organism="unknown"
BASE COUNT 7 a 20 c 9 g 3 t
ORIGIN

Alignment Scores:
Pred. No.: 4.61e+03 Length: 39
Score: 63.00 Matches: 11
Percent Similarity: 91.67% Conservative: 0
Best Local Similarity: 91.67% Mismatches: 1
Query Match: 5.71% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR020782 (1-24)

QY 188 TrpIleGlnAspAsnGlyGlyTrp 195
24 TGGATHCARGAAYAGGNGGNTGG 1
RESULT 7
AR052606 AR052606 33 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 4 from patent US 5831066.
ACCESSION AR052606
VERSION AR052606.1 GI:5975970
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 4 03-NOV-1998;
FEATURES Location/Qualifiers
source
1..33
BASE COUNT 5 a 5 c 16 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 3.4e+04 Length: 33
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.26% Indels: 0
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR052606 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200
10 GGAGGCTGGGTAGGTGCATCTGGT 33
RESULT 8
I96085 I96085 33 bp DNA linear PAT 01-DEC-1998
LOCUS
DEFINITION Sequence 4 from patent US 5734033.
ACCESSION I96085
VERSION I96085.1 GI:3940555
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 4 31-MAR-1998;
FEATURES Location/Qualifiers
source
1..33
BASE COUNT 5 a 5 c 16 g 7 t
ORIGIN

Alignment Scores:
Pred. No.: 3.4e+04 Length: 33
Score: 47.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00%  
Query Match: 4.26%  
DB: 6  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-375-514-22 (1-205) x I96085 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200  
Db 10 GGAGGCTGGGTAGGTGCATCTGCT 33

RESULT 9  
AR007294

LOCUS AR007294 28 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 8 from patent US 5750390.

ACCESSION AR007294  
VERSION AR007294.1 GI:3966778

KEYWORDS  
SOURCE Unknown.

ORGANISM  
Unclassified.

REFERENCE 1 (bases 1 to 28)

AUTHORS Thompson,J.D. and Draper,K.G.

TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene

JOURNAL Patent: US 5750390-A 8 12-MAY-1998;

FEATURES Location/Qualifiers

1..28

/organism="unknown"

BASE COUNT 3 a 13 c 7 g 5 t

ORIGIN

Alignment Scores:

Pred. No.: 3.81e+04 Length: 28

Score: 45.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 4.08% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR007294 (1-28)

QY 91 ProValValHisLeuAlaLeuArgGln 99

Db 1 CCTGTGGTCCACCTGGCCCTCCGCCAA 27

RESULT 10

HSJ5138/c

LOCUS HSJ5138 36 bp DNA linear PRI 27-AUG-1998

DEFINITION Homo sapiens CBS gene, intron 7, 5' end.

ACCESSION AJ005138

VERSION AJ005138.1 GI:3451235

KEYWORDS CBS gene; cystathionine beta-synthase.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 36)

AUTHORS Gaustadnes,M.

TITLE Direct Submission

JOURNAL Submitted (21-APR-1998) Gaustadnes M., Department of Clinical Biochemistry, Skejby University Hospital, Brendstrupgaardsvej, 8200 Aarhus N, DENMARK

REFERENCE 2 (bases 1 to 36)

AUTHORS Kraus,J.P., Le.K., Swaroop,M., Ohura,T., Tahara,T., Rosenberg,I.E., Roper,M.D. and Kozlich,V.

TITLE Human cystathionine beta-synthase cDNA: sequence, alternative splicing and expression in cultured cells

JOURNAL Hum. Mol. Genet. 2 (10), 1633-1638 (1993)

MEDLINE 94093551

PUBMED 7903580

REFERENCE 3 (bases 1 to 36)

AUTHORS Gaustadnes,M., Kluijtmans,L.A., Jensen,O.K., Rasmussen,K., Heil,S.G., Kraus,J.P., Blom,H.J., Ingerslev,J. and Rudiger,N.

TITLE Detection of a novel deletion in the cystathionine beta-synthase (CBS) gene using an improved genomic DNA based method

JOURNAL FEBS Lett. 431 (2), 175-179 (1998)

MEDLINE 98372628

PUBMED 9708897

FEATURES Location/Qualifiers

1..36

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="21"

/map="q22.3"

1..36

/gene="CBS"

<1..6

/gene="CBS"

/number=7

7..>36

/gene="CBS"

/number=7

BASE COUNT 4 a 6 c 21 g 5 t

ORIGIN

Alignment Scores:

Pred. No.: 4.8e+04 Length: 36

Score: 45.00 Matches: 7

Percent Similarity: 88.89% Conservative: 1

Best Local Similarity: 77.78% Mismatches: 1

Query Match: 4.08% Indels: 0

DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x HSAJ5138 (1-36)

QY 52 GlnProGlyHisThrProHisProAla 60

Db 27 CGGCCCGGCCACACCTCACCCTGCA 1

RESULT 11

LOCUS AR053546 24 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 11 from patent US 5834248.

ACCESSION AR053546

VERSION AR053546.1 GI:5978408

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Falb,D.

TITLE Compositions and methods using rchd534, a gene upregulated by shear stress

JOURNAL Patent: US 5834248-A 11 10-NOV-1998;

FEATURES Location/Qualifiers

1..24

/organism="unknown"

BASE COUNT 4 a 14 c 1 g 5 t

ORIGIN

Alignment Scores:

Pred. No.: 3.77e+04 Length: 24

Score: 44.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.99% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR053546 (1-24)

QY 140 AspGlyValAsnTrpGlyArg 146

Db 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 12

AR065873/c

LOCUS AR065873 24 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5849578.  
ACCESSION AR065873  
VERSION AR065873.1 GI:5996089  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd528 as a target  
JOURNAL Patent: US 5849578-A 11 15-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..24  
BASE COUNT 4 a 14 c 1 g 5 t  
ORIGIN  
Alignment Scores: 3.77e+04 Length: 24  
Pred. No.: 44.00 Matches: 7  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 3.99% Indels: 0  
Query Match: 3.99% Gaps: 0  
DB:  
US-09-375-514-22 (1-205) x AR065873 (1-24)  
QY 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGAGG 3  
RESULT 13  
AR080355/C  
LOCUS AR080355 24 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 11 from patent US 5968770.  
ACCESSION AR080355  
VERSION AR080355.1 GI:10007090  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd523 as a target  
JOURNAL Patent: US 5968770-A 11 19-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..24  
BASE COUNT 4 a 14 c 1 g 5 t  
ORIGIN  
Alignment Scores: 3.77e+04 Length: 24  
Pred. No.: 44.00 Matches: 7  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 3.99% Indels: 0  
Query Match: 3.99% Gaps: 0  
DB:  
US-09-375-514-22 (1-205) x AR080355 (1-24)  
QY 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGAGG 3  
RESULT 14  
AR148310/C  
LOCUS AR148310 24 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 11 from patent US 6225084.  
ACCESSION AR148310

VERSION ARL48310.1 GI:15112400  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd534 as a target  
JOURNAL Patent: US 6225084-A 11 01-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..24  
BASE COUNT 4 a 14 c 1 g 5 t  
ORIGIN  
Alignment Scores: 3.77e+04 Length: 24  
Pred. No.: 44.00 Matches: 7  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 3.99% Indels: 0  
Query Match: 3.99% Gaps: 0  
DB:  
US-09-375-514-22 (1-205) x ARL48310 (1-24)  
QY 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGAGG 3  
RESULT 15  
AX031294  
LOCUS AX031294 28 bp DNA linear PAT 20-SEP-2000  
DEFINITION Sequence 16 from Patent WO9914321.  
ACCESSION AX031294  
VERSION AX031294.1 GI:10278622  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S., Huang,D.C. and Strasser,A.  
TITLE Novel therapeutic molecules  
JOURNAL Patent: WO 9914321-A 16 25-MAR-1999;  
INST MEDICAL W & E HALL (AU); PUTHALAKATH HAMSA (AU); REILLY LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU)  
FEATURES Location/Qualifiers  
source 1..28  
BASE COUNT 8 a 11 c 6 g 3 t  
ORIGIN  
Alignment Scores: 4.95e+04 Length: 28  
Pred. No.: 43.00 Matches: 8  
Score: 88.89% Conservative: 0  
Percent Similarity: 88.89% Mismatches: 1  
Best Local Similarity: 3.89% Indels: 0  
Query Match: 3.89% Gaps: 0  
DB:  
US-09-375-514-22 (1-205) x AX031294 (1-28)  
QY 184 HisLeuHisThrTrpIleGlnAspAsn 192  
Db 1 CACCTGCACACCGCATCCAGGATAAC 27  
RESULT 16  
AX031320  
LOCUS AX031320 28 bp DNA linear UNA 20-SEP-2000  
DEFINITION Sequence 16 from Patent WO9914321.

ACCESSION AX031320  
VERSION AX031320.1 GI:10278645  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS O'Reilly,L., Puthalakath,H., Adams,J., O'Connor,L., Cory,S.,  
Huang,D.C. and Strasser,A.  
TITLE Novel therapeutic molecules  
JOURNAL Patent: WO 9914321-A 25-MAR-1999;  
INST MEDICAL W & E HALL (AU) ; PUTHALAKATH HAMSA (AU) ; REILLY  
LORRAINE O (AU) ; ADAMS JERRY (AU) ; CONNOR LIAM O (AU) ; CORY  
SUZANNE (AU) ; HUANG DAVID C S (AU) ; STRASSER ANDREAS (AU)

FEATURES  
source  
1. .28  
/organism="unidentified"  
/db\_xref="taxon:32644" 3 t

BASE COUNT 8 a 11 c 6 g 3 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4.95e+04 Length: 28  
Score: 43.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 3.89% Indels: 0  
DB: 13 Gaps: 0

US-09-375-514-22 (1-205) x AX031320 (1-28)

QY 184 HistLeuHsHrTpIleGlnAspAsn 192  
Db 1 CACCTGCACACCCGGATCCAGGATAC 27

RESULT 17  
AR090476/c  
LOCUS AR090476 25 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 596 from patent US 5994076.  
ACCESSION AR090476  
VERSION AR090476.1 GI:10017231  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 596 30-NOV-1999;  
FEATURES  
source  
1. .25  
/organism="unknown"  
5 a 11 c 4 g 5 t

Alignment Scores:  
Pred. No.: 5.09e+04 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR090476 (1-25)

QY 189 IleGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCAGGTTGGTGGTG 1

RESULT 18  
AR197511/c  
LOCUS AR197511 31 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 596 from patent US 6352829.

ACCESSION AR197511  
VERSION AR197511.1 GI:20247360  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 6352829-A 596 05-MAR-2002;  
FEATURES  
source  
1. .25  
/organism="unknown"  
5 a 11 c 4 g 5 t

BASE COUNT 5 a 11 c 4 g 5 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5.09e+04 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AR197511 (1-25)

QY 189 IleGlnAspAsnGlyGlyTrpVal 196  
Db 24 ATCCAAGACCAGGTTGGTGGTG 1

RESULT 19  
I60569  
LOCUS I60569 39 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 21 from patent US 5656725.  
ACCESSION I60569  
VERSION I60569.1 GI:2479014  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)  
AUTHORS Chittenden,T.D. and Lutz,R.J.  
TITLE Peptides and compositions which modulate apoptosis  
JOURNAL Patent: US 5656725-A 21 12-AUG-1997;  
FEATURES  
source  
1. .39  
/organism="unknown"  
11 a 11 c 11 g 6 t

BASE COUNT 11 a 11 c 11 g 6 t  
ORIGIN

Alignment Scores:  
Pred. No.: 7.72e+04 Length: 39  
Score: 42.00 Matches: 7  
Percent Similarity: 75.00% Conservative: 2  
Best Local Similarity: 58.33% Mismatches: 3  
Query Match: 3.80% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I60569 (1-39)

QY 101 GlyAspAspPheSerArgTyrArgGlyAspPhe 112  
Db 1 GGGGACGACATCATCCAGCGCTATGACTCAGAGTTTC 36

RESULT 20  
AX022526/c  
LOCUS AX022526 31 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 3 from Patent EP0932674.  
ACCESSION AX022526  
VERSION AX022526.1 GI:10046124  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

unclassified.  
 1 (bases 1 to 31)  
 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
 A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
 apoptosis-controlling genes  
 JOURNAL Patent: EP 0932674-A 3 04-AUG-1999;  
 AMRAD OPERATIONS PTY LTD (AU)  
 FEATURES Location/Qualifiers  
 source 1..31  
 /organism="unidentified"  
 /db\_xref="taxon:32644"  
 14  
 /note="INOSINE (I)"  
 17  
 /note="INOSINE (I)"  
 20  
 /note="INOSINE (I)"  
 5 a 10 c 5 g 7 t 4 others

BASE COUNT 5 a 10 c 5 g 7 t 4 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7.12e+04 Length: 31  
 Score: 41.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 3.71% Indels: 0  
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX022526 (1-31)

Qy 188 TrpIleGlnAspAsnGlyGlyTrp 195  
 |||||  
 Db 31 TGGATCCAGANMANGNGGCTGG 8

RESULT 21  
 AX030814/c  
 LOCUS 31 bp DNA linear PAT 20-SEP-2000  
 DEFINITION Sequence 3 from Patent WO9735971.  
 ACCESSION AX030814  
 VERSION AX030814.1 GI:10278310  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unclassified

REFERENCE 1 (bases 1 to 31)  
 Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
 A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
 apoptosis-controlling genes  
 Patent: WO 9735971-A 3 02-OCT-1997;  
 JOURNAL ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)  
 ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)  
 FEATURES Location/Qualifiers  
 source 1..31  
 /organism="unidentified"  
 /db\_xref="taxon:32644"  
 14  
 /mod\_base-i  
 17  
 /mod\_base-i  
 20  
 /mod\_base-i  
 5 a 10 c 5 g 7 t 4 others

BASE COUNT 5 a 10 c 5 g 7 t 4 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7.12e+04 Length: 31  
 Score: 41.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 3.71% Indels: 0  
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX030814 (1-31)

Qy 188 TrpIleGlnAspAsnGlyGlyTrp 195  
 |||||  
 Db 31 TGGATCCAGANMANGNGGCTGG 8

RESULT 22  
 I89980  
 LOCUS 33 bp DNA linear PAT 10-AUG-1998  
 DEFINITION Sequence 28 from patent US 5723318.  
 ACCESSION I89980  
 VERSION I89980.1 GI:3409920  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 33)  
 YAMAGUCHI,N., KOJIMA,T., OH-EDA,M. and HATTORI,K.  
 DNA coding for megakaryocyte potentiator  
 JOURNAL Patent: US 5723318-A 28 03-MAR-1998;  
 FEATURES Location/Qualifiers  
 source 1..33  
 /organism="unknown"  
 1 a 13 c 14 g 5 t

BASE COUNT 1 a 13 c 14 g 5 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7.55e+04 Length: 33  
 Score: 41.00 Matches: 8  
 Percent Similarity: 80.00% Conservative: 0  
 Best Local Similarity: 80.00% Mismatches: 2  
 Query Match: 3.71% Indels: 0  
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I89980 (1-33)

Qy 76 AlaAlaProGlyAlaAlaGlyProAla 85  
 |||||  
 Db 3 GCGGGCGCTGGTGGCTGGTGGCGCCAGCC 32

RESULT 23  
 S80834/c  
 LOCUS 33 bp DNA linear PRI 07-MAY-1993  
 DEFINITION gamma delta T cell antigen receptor delta-chain [V delta 2-J delta  
 1 junction] [human, skin lesion, Genomic, 33 nt].  
 ACCESSION S80834  
 VERSION S80834.1 GI:245000  
 KEYWORDS  
 SOURCE Homo sapiens skin lesion.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Uyemura,K., Klotz,J., Pirmez,C., Ohmen,J., Wang,X.H., Ho,C.,  
 Hoffman,W.L. and Modlin,R.L.  
 TITLE Microanatomic clonality of gamma delta T cells in human  
 JOURNAL leishmaniasis lesions  
 MEDLINE J. Immunol. 148 (4), 1205-1211 (1992)  
 PUBMED 92148143  
 1531352

REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 80834] from the original journal article.  
 This sequence comes from Figure 4.

FEATURES Location/Qualifiers  
 source 1..33  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 1..33  
 /partial

gene

BASE COUNT 10 a 7 c 10 g 6 t  
 ORIGIN

Alignment Scores:



Pred. No.: 7.55e+04 33 Length: 33  
Score: 41.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.71% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x S80834 (1-33)

Qy 88 ProValProProValValHis 94

Db 21 OCTGTACCCCGAGTAGTTCAC 1  
|||||

RESULT 24

LOCUS 165770/c 36 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 6 from patent US 5668294.

ACCESSION I65770

VERSION I65770.1 GI:2482340

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 36)

AUTHORS Meagher, R.B. and Summers, A.O.

TITLE Metal resistance sequences and transgenic plants

JOURNAL Patent: US 5668294-A 6 16-SEP-1997;

FEATURES Location/Qualifiers

source 1..36

BASE COUNT 8 a 13 c 9 g 6 t

ORIGIN

Alignment Scores:

Pred. No.: 8.19e+04 36 Length: 36

Score: 41.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 3.71% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I65770 (1-36)

Qy 75 ProAlaProGlyAlaAlaAGly 83

Db 35 CCTGCTGCGCGGAGGCTGCAGGA 9  
|||||

RESULT 25

LOCUS AR168776/c 38 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 2 from patent US 6288042.

ACCESSION AR168776

VERSION AR168776.1 GI:17904871

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Ojwang, J.O., Hogan, M.E., Wallace, T.L. and Cossun, P.A.

TITLE Anti-viral guanidine-rich tetrad forming oligonucleotides

JOURNAL Patent: US 6288042-A 2 11-SEP-2001;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:

Pred. No.: 8.61e+04 38 Length: 38

Score: 41.00 Matches: 8

Percent Similarity: 50.00% Conservative: 0

Best Local Similarity: 50.00% Mismatches: 2

Query Match: 3.71% Indels: 6

DB: 6 Gaps: 1  
US-09-375-514-22 (1-205) x AR168776 (1-38)  
Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59  
Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3  
|||||

RESULT 26

AR200245/c

LOCUS AR200245 38 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 2 from patent US 6355785.

ACCESSION AR200245

VERSION AR200245.1 GI:20250319

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Fennelwald, S., Zendeigui, J.G., Ojwang, J.O., Hogan, M.E.,

Pommier, Y., and Mazumder, A.

TITLE Guanidine-rich oligonucleotide integrase inhibitors

JOURNAL Patent: US 6355785-A 2 12-MAR-2002;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:

Pred. No.: 8.61e+04 38 Length: 38

Score: 41.00 Matches: 8

Percent Similarity: 50.00% Conservative: 0

Best Local Similarity: 50.00% Mismatches: 2

Query Match: 3.71% Indels: 6

DB: 6 Gaps: 1

US-09-375-514-22 (1-205) x AR200245 (1-38)

Qy 44 ProAlaProGlyIlePheSerGlnProGlyHisThrProHisPro 59

Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCC 3  
|||||

RESULT 27

I27770/c

LOCUS I27770 38 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 2 from patent US 5567604.

ACCESSION I27770

VERSION I27770.1 GI:1818546

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 38)

AUTHORS Rando, R.F., Fennelwald, S., Zendeigui, J.G. and Ojwang, J.O.

TITLE Anti-viral guanidine-rich oligonucleotides

JOURNAL Patent: US 5567604-A 2 22-OCT-1996;

FEATURES Location/Qualifiers

source 1..38

BASE COUNT 0 a 0 c 29 g 9 t

ORIGIN

Alignment Scores:

Pred. No.: 8.61e+04 38 Length: 38

Score: 41.00 Matches: 8

Percent Similarity: 50.00% Conservative: 0

Best Local Similarity: 50.00% Mismatches: 2

Query Match: 3.71% Indels: 6

DB: 6 Gaps: 1

US-09-375-514-22 (1-205) x I27770 (1-38)

Qy 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59  
Db 32 CCCACCCA-----CCCCCCCCACACCCACACCC 3

## RESULT 28

A47631 LOCUS A47631 35 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 8 from Patent EP0699755.  
ACCESSION A47631  
VERSION A47631.1 GI:2301576

KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.

## REFERENCE

1 (bases 1 to 35)  
Rodriguez,R.P., Valladares,J.L. and Mateo,D.A.  
TITLE Method for obtaining modified immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them

## JOURNAL

Patient: EP 0699755-A 8 06-MAR-1996;  
IMMUNOLOGIA MOLECULAR CENTRO (CU)

## COMMENT

Other publication CA 2153135 951231.

## FEATURES

source 1..35  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 6 a 14 c 8 g 7 t

## ORIGIN

Alignment Scores:  
Pred. No.: 9.11e+04 Length: 35  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A47631 (1-35)

Qy 45 AlaProGlyIlePheSerSerGlnProGly 54

Db 4 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 33

## RESULT 29

I82275 LOCUS I82275 35 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 8 from patent US 5712120.  
ACCESSION I82275  
VERSION I82275.1 GI:3210572

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

## REFERENCE

1 (bases 1 to 35)  
Rodriguez,R.Perez., Mateo de Acosta del Rio,C.Maria. and  
Valladares,J.Lombardero.

TITLE Method for obtaining modified immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them

## JOURNAL

Patient: US 5712120-A 8 27-JAN-1998;  
Location/Qualifiers

## FEATURES

source 1..35  
/organism="unknown"  
/db\_xref="taxon:32644"

BASE COUNT 6 a 14 c 8 g 7 t

## ORIGIN

Alignment Scores:  
Pred. No.: 9.11e+04 Length: 35  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I82275 (1-35)

Qy 45 AlaProGlyIlePheSerSerGlnProGly 54

Db 4 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 33

## RESULT 30

A47633 LOCUS A47633 36 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 10 from Patent EP0699755.  
ACCESSION A47633  
VERSION A47633.1 GI:2301578

KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.

## REFERENCE

1 (bases 1 to 36)  
Rodriguez,R.P., Valladares,J.L. and Mateo,D.A.

TITLE Method for obtaining modified immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them

## JOURNAL

Patient: EP 0699755-A 10 06-MAR-1996;  
IMMUNOLOGIA MOLECULAR CENTRO (CU)

## COMMENT

Other publication CA 2153135 951231.

## FEATURES

source 1..36  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 8 a 8 c 14 g 6 t

## ORIGIN

Alignment Scores:  
Pred. No.: 9.36e+04 Length: 36  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A47633 (1-36)

Qy 45 AlaProGlyIlePheSerSerGlnProGly 54

Db 32 GCCCAGGCTTCTTCACTTCAGCCCGAGGC 3

## RESULT 31

A68670 LOCUS A68670 36 bp DNA linear PAT 06-MAY-1999  
DEFINITION Sequence 16 from Patent WO9801550.  
ACCESSION A68670  
VERSION A68670.1 GI:4759684

KEYWORDS  
SOURCE unidentified.  
ORGANISM unclassified.

## REFERENCE

1 (bases 1 to 36)  
Cornelissen,A.W. and Schallig,H.D.

TITLE VACCINE AGAINST GASTRO-INTESTINAL NEMATODES

JOURNAL Patent: WO 9801550-A 16 15-JAN-1998;  
UNIV UTRECHT (NL)

## FEATURES

source 1..36  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 10 a 4 c 15 g 7 t

## ORIGIN

Alignment Scores:  
Pred. No.: 9.36e+04 Length: 36  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1

Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A68670 (1-36)

Qy 27 GlyTyrGluTrpAspAlaGly 33  
|||||  
Db 10 GGATACGAATGGGATGAGGA 30

RESULT 32  
182277/c  
LOCUS Sequence 10 from patent US 5712120. 36 bp DNA linear PAT 10-JUN-1998  
DEFINITION  
ACCESSION I82277  
VERSION I82277.1 GI:3210574  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 36)  
Rodriguez,R.Perez., Mateo de Acosta del Rio,C.Maria. and Valladares,J.Lombardero.  
TITLE Method for obtaining modified immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them  
JOURNAL Patent: US 5712120-A 10 27-JAN-1998;  
FEATURES Location/Qualifiers  
source 1..36  
BASE COUNT 8 a 8 c 14 g 6 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9.36e+04 Length: 36  
Score: 40.00 Matches: 7  
Percent Similarity: 80.00% Conservative: 1  
Best Local Similarity: 70.00% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x I82277 (1-36)

Qy 45 AlaProGlyIlePheSerSerGlnProGly 54  
|||||  
Db 32 GCCCAGGCTCTTCACTTCAGCCCGCCAGC 3

RESULT 33  
AR096669  
LOCUS Sequence 7 from patent US 6008193. 40 bp DNA linear PAT 08-SEP-2000  
DEFINITION  
ACCESSION AR096669  
VERSION AR096669.1 GI:10025673  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Garfinkel,J. and Richter,T.  
TITLE Methods of using human von Willebrand factor GPIb binding domain polypeptides  
JOURNAL Patent: US 6008193-A 7 28-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..40  
BASE COUNT 11 a 14 c 8 g 7 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.03e+05 Length: 40  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0

US-09-375-514-22 (1-205) x AR096669 (1-40)

Qy 53 ProGlyHisThrProHisPro 59  
|||||  
Db 1 CCAGCAGCAACGCCACATCCA 21

RESULT 34  
AX262441/c  
LOCUS Sequence 16 from Patent WO0172119. 40 bp DNA linear PAT 26-OCT-2001  
DEFINITION  
ACCESSION AX262441  
VERSION AX262441.1 GI:16511355  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Cornali,E., Nehls,M.C., Schlueter,V., Wattler,F., Wattler,S. and Wolf,S.  
TITLE Non-human animal model for growth deficiency and information processing or cognitive function defects and use thereof  
JOURNAL Patent: WO 0172119-A 16 04-OCT-2001;  
Ingenium Pharmaceuticals AG (DE)  
FEATURES Location/Qualifiers  
source 1..40  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"  
BASE COUNT 5 a 15 c 16 g 4 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.03e+05 Length: 40  
Score: 40.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 3.62% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX262441 (1-40)

Qy 33 GlyAspValGlyAlaAlaProGly 41  
|||||  
Db 40 GGAGACTCGGAGCTGTGCTCCCGC 14

RESULT 35  
AX248386  
LOCUS Sequence 465 from Patent WO0166800. 31 bp DNA linear PAT 28-SEP-2001  
DEFINITION  
ACCESSION AX248386  
VERSION AX248386.1 GI:15863009  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0166800-A 465 13-SEP-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES Location/Qualifiers  
source 1..31  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 8 a 7 c 8 g 7 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 9.3e+04 Length: 31  
Score: 39.00 Matches: 5





JOURNAL Patent: WO 9910529-A 2 04-MAR-1999;  
MORTEN JOHN EDWARD NORRIS (GB); ZENECA LTD (GB)

## FEATURES

source Location/Qualifiers

1..30 /organism="unidentified"  
/db\_xref="taxon:32644" 1 t

## BASE COUNT

ORIGIN 2 a 9 c 18 g 1 t

## Alignment Scores:

Pred. No.: 1.03e+05 Length: 30  
Score: 38.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.44% Indels: 0  
DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A98608 (1-30)

38 AlaProGlyAlaAlaProAla 45

Db 29 GCCCGCTGGAGCGCCCGGCC 6

## RESULT 44

S66556

LOCUS

DEFINITION S66556 30 bp DNA linear PRI 05-MAY-2000  
COLL1A1-collagen alpha 1(I) chain [exon 43] [human, Genomic Mutant,  
30 nt].

ACCESSION S66556

VERSION S66556.1 GI:239218

KEYWORDS

SOURCE Homo sapiens:

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 30)

TITLE Hawkins, J.R., Superti-Furga, A., Steinmann, B. and Dalglish, R.

JOURNAL A 9-base pair deletion in COL1A1 in a lethal variant of

MEDLINE osteogenesis imperfecta

PUBMED 92042176

REMARK J. Biol. Chem. 266 (33), 22370-22374 (1991)

GenBank staff at the National Library of Medicine created this

entry [NCBI gibseq 66556] from the original journal article.

This sequence comes from Figure 3.

## FEATURES

source

1..30 Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

<1..>30

/gene="COL1A1"

/note="collagen alpha 1(I) chain"

<1..>30

/note="This sequence comes from Figure 3; 9 base pair

deletion; conceptual translation presented here differs

from translation in publication"

/codon\_start=1

/product="collagen alpha 1(I) chain"

/protein\_id="AAB20361.1"

/db\_xref="GI:239219"

/translation="GPPGAPGAPG"

1 a 13 c 10 g 6 t

## BASE COUNT

ORIGIN

## Alignment Scores:

Pred. No.: 1.03e+05 Length: 30  
Score: 38.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 3.44% Indels: 0  
DB: 9 Gaps: 0

US-09-375-514-22 (1-205) x S66556 (1-30)

QY 39 ProGlyAlaAlaProAlaProGly 47

Db 4 CCCCCTGGTCTCTCTGGTCCCCCTGGC 30

## RESULT 45

AX248864/c

LOCUS

DEFINITION AX248864 31 bp DNA linear PAT 28-SEP-2001

SEQUENCE 943 from Patent WO0166800.

ACCESSION AX248864

VERSION AX248864.1 GI:15863487

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 31)

TITLE Cargill, M., Ireland, J.S. and Lander, E.S.

JOURNAL Human single nucleotide polymorphisms

Patent: WO 0166800-A 943 13-SEP-2001;

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES Location/Qualifiers

1..31

source /organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 5 a 10 c 13 g 2 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05 Length: 31

Score: 38.00 Matches: 6

Percent Similarity: 87.50% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX248864 (1-31)

QY 40 ProGlyAlaAlaProAlaProGly 47

Db 31 CCAGGGTCGCTCCACCCCTGGG 8

## RESULT 46

AX477731

LOCUS

DEFINITION AX477731 31 bp DNA linear PAT 12-AUG-2002

SEQUENCE 13 from Patent WO0240530.

ACCESSION AX477731

VERSION AX477731.1 GI:22216878

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE artificial sequences.

1

AUTHORS Fesik, S.W., Petros, A.M., Yoon, H. and Nettlesheim, D.G.

TITLE Mutant bcl-2 proteins and uses thereof

JOURNAL Patent: WO 0240530-A 13 23-MAY-2002;

ABBOTT LABORATORIES (US)

FEATURES Location/Qualifiers

1..31

source /organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Primer"

BASE COUNT 5 a 13 c 9 g 4 t

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05 Length: 31

Score: 38.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX477731 (1-31)

Qy 92 ValValHisLeuAlaLeuArgGlnAla 100  
 Db 4 GTGGTCCACCTGACCTCCGCCAAGCC 30

RESULT 47  
 AX477732/c

LOCUS AX477732 31 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 14 from Patent WO0240530.

ACCESSION AX477732

VERSION AX477732.1 GI:22216879

KEYWORDS synthetic construct.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Fesik, S.W., Petros, A.M., Yoon, H. and Nettesheim, D.G.

TITLE Mutant bcl-2 proteins and uses thereof

JOURNAL Patent: WO 0240530-A 14 23-MAY-2002;

ABBOTT LABORATORIES (US)

FEATURES Location/Qualifiers

source 1..31

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Primer"

BASE COUNT 4 a 9 c 13 g 5 t

ORIGIN

Alignment Scores:

Pred. No.: 1.06e+05 Length: 31

Score: 38.00 Matches: 8

Percent Similarity: 88.89% Conservativeness: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX477732 (1-31)

Qy 92 ValValHisLeuAlaLeuArgGlnAla 100

Db 28 GTGGTCCACCTGACCTCCGCCAAGCC 2

RESULT 48

A36722

LOCUS A36722 33 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 10 from Patent EP0586112.

ACCESSION A36722

VERSION A36722.1 GI:2293991

KEYWORDS Hepatitis C virus.

SOURCE Hepatitis C virus.

ORGANISM Hepatitis C virus.

REFERENCE 1 (bases 1 to 33)

AUTHORS Tercero, J.C., Garcia, L.C., Ramos, J.A. and Alemany, J.C.

TITLE Control of PCR mediated detection of micro-organisms

JOURNAL Patent: EP 0586112-A 10 09-MAR-1994;

PHARMA GEN S A (ES)

COMMENT Other publication JP 7087978 950404.

FEATURES Location/Qualifiers

source 1..33

/organism="Hepatitis C virus"

/db\_xref="taxon:11103"

BASE COUNT 8 a 11 c 8 g 6 t

ORIGIN

Alignment Scores:

Pred. No.: 1.13e+05 Length: 33

Score: 38.00 Matches: 8

Percent Similarity: 90.00% Conservativeness: 1

Best Local Similarity: 80.00% Mismatches: 1

Query Match: 3.44% Indels: 0  
 DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x A36722 (1-33)

Qy 60 AlaAlaSerArgAspProValAlaArgThr 69

Db 2 GCAGCTCCAGGATTCCAATTGCCAGGACG 31

RESULT 49

AX247606/c

LOCUS AX247606 38 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 27 from Patent WO0166804.

ACCESSION AX247606

VERSION AX247606.1 GI:15862295

KEYWORDS human.

SOURCE Homo sapiens

REFERENCE 1 (bases 1 to 38)

AUTHORS Cronin, M.T., Frueh, F. and Brennan, T.M.

TITLE Methods for optimizing hybridization performance of polynucleotide

JOURNAL probes and localizing and detecting sequence variations

FEATURES Patent: WO 0166804-A 27 13-SEP-2001;

Protogene Laboratories, Inc. (US)

Location/Qualifiers

source 1..38

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 8 a 7 c 16 g 7 t

ORIGIN

Alignment Scores:

Pred. No.: 1.28e+05 Length: 38

Score: 38.00 Matches: 7

Percent Similarity: 87.50% Conservativeness: 0

Best Local Similarity: 87.50% Mismatches: 1

Query Match: 3.44% Indels: 0

DB: 6 Gaps: 0

US-09-375-514-22 (1-205) x AX247606 (1-38)

Qy 83 GlyProAlaLeuSerProValPro 90

Db 36 GGTCCCGCACATACCACCGGTACCC 13

RESULT 50

AR052605/c

LOCUS AR052605 20 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 3 from patent US 5831066.

ACCESSION AR052605

VERSION AR052605.1 GI:5975969

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Reed, J.C.

TITLE Regulation of bcl-2 gene expression

JOURNAL Patent: US 5831066-A 3 03-NOV-1998;

Location/Qualifiers

source 1..20

/organism="unknown"

BASE COUNT 4 a 10 c 3 g 3 t

ORIGIN

Alignment Scores:

Pred. No.: 8.06e+04 Length: 20

Score: 37.00 Matches: 6

Percent Similarity: 100.00% Conservativeness: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.35% Indels: 0

DB: 6 Gaps: 0  
US-09-375-514-22 (1-205) x AR052605 (1-20)  
QY 193 GlyGlyTrpValcIyAia 198  
Db 20 GGAGGCTGGTAGGTGCA 3

Search completed: May 31, 2003, 22:59:21  
Job time : 1776 secs



GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 17:00:06 ; Search time 215 Seconds  
(without alignments)  
2147.254 Million cell updates/sec

Title: US-09-375-514-22

Perfect score: 1104

Sequence: 1 MAHAGRTGYDREIVMKYIH.....HTWIQDNGWVGASGDVSLG 205

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2056596

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q/cn2\_1/USFTO\_spool/US09375514/runat\_28052003\_165345\_18650/app\_query.fasta\_1.391  
-DB=N\_Geneseq\_101002 -QMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi  
-LIST=500 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=50  
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=10 -MAXLEN=40  
-USER=US09375514.@CN\_1.1.208.@runat\_28052003\_165345\_18650 -NCPU=6 -ICPU=3  
-NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	6.0	36	14	AAQ51961
2	57	5.2	33	14	AAQ51951
3	55	5.0	24	19	AAV28336
4	55	5.0	24	20	AAI15948
5	50	4.5	33	22	AAI64676
6	50	4.5	36	22	AAH45307
7	49	4.4	24	24	ABN85362
8	47	4.3	21	24	ABN85361
9	47	4.3	33	16	AAQ86646
10	47	4.3	33	19	AAV19654
11	47	4.3	33	24	ABL54152
12	45	4.1	28	14	AAQ51954
13	44	4.0	24	17	AAI36054
14	44	4.0	24	20	AAI36054
15	44	4.0	24	20	AAI36054
16	44	4.0	24	20	AAI36054
17	44	4.0	24	21	AAI36054
18	44	4.0	24	21	AAI36054
19	44	4.0	24	21	AAI36054
20	44	4.0	24	21	AAI36054
21	44	4.0	24	21	AAI36054
22	42	3.8	25	24	ABK66508
23	42	3.8	27	22	AAH45298
24	42	3.8	27	22	AAH45302
25	42	3.8	39	17	AAI42430
26	42	3.8	39	24	ABK11179
27	41	3.7	27	22	AAH45299
28	41	3.7	27	22	AAH45306
29	41	3.7	31	18	AAI96580
30	41	3.7	36	18	AAI92245
31	41	3.7	36	20	AAI28595
32	41	3.7	38	14	AAQ41913
33	41	3.7	38	15	AAQ44773
34	41	3.7	38	15	AAQ79202
35	41	3.7	38	18	AAI51620
36	41	3.7	38	19	AAI79211
37	41	3.7	38	16	AAQ95496
38	40	3.6	24	24	ABK52487
39	40	3.6	27	17	AAI08792
40	40	3.6	27	22	AAH45300
41	40	3.6	40	12	AAQ13427
42	40	3.6	40	20	AAV74159
43	40	3.6	40	20	AAV08903
44	40	3.6	40	21	AAI56179
45	40	3.6	40	22	AAI17995
46	40	3.6	40	23	AAI46236
47	39	3.5	23	21	AAI26253
48	39	3.5	23	21	AAI26253
49	39	3.5	23	22	AAH45301
50	39	3.5	27	22	AAH45303
51	39	3.5	27	22	AAH45304
52	39	3.5	32	20	AAH45497
53	39	3.5	32	21	AAI20548
54	39	3.5	32	21	AAI20548
55	39	3.5	33	21	AAI20547
56	39	3.5	33	21	AAI20547
57	39	3.5	33	21	AAI20547
58	39	3.5	34	21	AAI20547
59	39	3.5	34	21	AAI20547
60	39	3.5	34	21	AAI20547
61	39	3.5	35	21	AAI20547
62	39	3.5	35	21	AAI20547
63	39	3.5	35	21	AAI20547
64	39	3.5	35	21	AAI20547
65	39	3.5	36	20	AAI20547
66	39	3.5	36	21	AAI20544
67	39	3.5	36	21	AAI20544

68	39	3.5	37	20	AA54974	C/EBP-beta antisen	c 141	36	3.3	20	22	AA515195	Human bcl-x antise
69	39	3.5	37	21	AA54974	Human C/EBP polyu	c 142	36	3.3	20	22	AA515195	Human bcl-x antise
70	39	3.5	37	21	AA54974	Human adenosine re	c 143	36	3.3	20	24	AB196903	Capture oligonucle
71	39	3.5	38	20	AA54973	C/EBP-beta antisen	c 144	36	3.3	23	14	AA051950	BCL-2 mRNA ribozym
72	39	3.5	38	21	AA54973	Human C/EBP polyu	c 145	36	3.3	24	24	AB190376	Capture oligonucle
73	39	3.5	38	21	AA54973	Human adenosine re	c 146	36	3.3	24	24	AB190377	Capture oligonucle
74	39	3.5	39	13	AAQ20998	DNA probe pl-79.	c 147	36	3.3	25	24	AB199998	Left PCR primer us
75	39	3.5	39	20	AA54972	C/EBP-beta antisen	c 148	36	3.3	25	24	ABN04782	Human GMMLP-1 25-m
76	39	3.5	39	21	AA54972	Human C/EBP polyu	c 149	36	3.3	25	24	ABN04783	Human GMMLP-1 25-m
77	39	3.5	39	21	AA54972	Human adenosine re	c 150	36	3.3	25	24	ABN04784	Human GMMLP-1 25-m
78	39	3.5	40	16	AA54971	Oligonucleotide #H	c 151	36	3.3	25	24	ABN04785	Human GMMLP-1 25-m
79	39	3.5	40	20	AA54971	C/EBP-beta antisen	c 152	36	3.3	25	24	ABN04786	Human GMMLP-1 25-m
80	39	3.5	40	21	AA54971	Human C/EBP polyu	c 153	36	3.3	25	24	ABN04787	Human GMMLP-1 25-m
81	39	3.5	40	21	AA54971	Human adenosine re	c 154	36	3.3	25	24	ABN04788	Human GMMLP-1 25-m
82	39	3.5	40	22	AA54972	Mouse kappa light	c 155	36	3.3	25	24	ABN04789	Human GMMLP-1 25-m
83	38.5	3.5	31	22	AA129884	Human single nucle	c 156	36	3.3	27	24	ABK52426	Human FGF-related
84	38	3.4	20	22	AA129884	Human Bcl-2 protei	c 157	36	3.3	28	15	AAQ79214	Guanosine rich oli
85	38	3.4	20	22	AA129884	Human Bcl-2 protei	c 158	36	3.3	29	24	ABK49675	Mouse intron 1 3'
86	38	3.4	22	21	AA54971	BCL2 RNA RT-PCR pr	c 159	36	3.3	30	16	AAQ99758	Primer #1 for ampl
87	38	3.4	24	21	AA54971	BCL-2 PCR primer #	c 160	36	3.3	30	21	AAQ99758	Multiplex analysis
88	38	3.4	24	22	AA54971	Human BCL-2 PCR pr	c 161	36	3.3	30	21	AAQ99758	PCR primer for mou
89	38	3.4	24	22	AA54971	Diagnostic primer	c 162	36	3.3	30	22	AA48653	Human haemochromat
90	38	3.4	30	20	AA54971	Human single nucle	c 163	36	3.3	30	22	AA48653	Haemochromatosis s
91	38	3.4	31	22	AA129977	Human single nucle	c 164	36	3.3	30	23	AA515717	Otoferlin exon/int
92	38	3.4	33	15	AAQ56297	Matagenic primer M	c 165	36	3.3	30	23	AA515717	Human genomic DNA
93	38	3.4	36	19	AA54971	Human bak BH2 doma	c 166	36	3.3	31	21	AAQ78940	Human single nucle
94	38	3.4	37	24	AA54971	Penton-base adenov	c 167	36	3.3	31	22	AA130727	5' primer for CD34
95	38	3.4	38	22	AA54971	Beta actin gene pr	c 168	36	3.3	32	17	AAQ46094	Human G protein co
96	38	3.4	38	24	AA54971	Human wt1 truncati	c 169	36	3.3	32	18	AAQ46094	Human ECD-deltaPD
97	37	3.4	20	19	AA54971	Human bcl-2 antise	c 170	36	3.3	32	21	AAQ89741	Human Her-2/neu EC
98	37	3.4	20	21	AA54971	PCR primer for hum	c 171	36	3.3	32	24	ABQ22527	Molecular stick DN
99	37	3.4	20	24	AA54971	Bcl-2 antisenase ol	c 172	36	3.3	33	10	AAQ91503	Thrombin receptor
100	37	3.4	24	21	AA54971	Brevibacterium lac	c 173	36	3.3	35	22	AAQ30201	fdTetBSN vector ol
101	37	3.4	24	21	AA54971	PCR primer used to	c 174	36	3.3	38	13	AAQ28347	DNA PCR primer RA0
102	37	3.4	24	24	ABK15648	Bcl-2 RNA-DNA hybr	c 175	36	3.3	38	14	AAQ37106	Probe for bovine t
103	37	3.4	28	14	AAQ46987	First type III-C a	c 176	36	3.3	38	21	AAQ68521	E-cadherin SNP pro
104	37	3.4	28	18	AAQ71141	Fibronectin fragme	c 177	36	3.3	38	21	AAQ68521	Reporter vector in
105	37	3.4	28	19	AAQ28773	Fibronectin PCR 3'	c 182	36	3.3	39	17	AAQ39129	IL-4 2'F/NH2 RNA 1
106	37	3.4	28	20	AAQ59809	Human fibronectin	c 183	36	3.3	39	18	AAQ7275	Primer JSS33(B) us
107	37	3.4	29	20	AA54982	C/EBP-beta antisen	c 184	36	3.3	39	21	AAQ29474	Human IL4Ralpha ge
108	37	3.4	29	21	AA54982	Human C/EBP polyu	c 185	36	3.3	39	22	AAQ69839	Corn male reproduc
109	37	3.4	29	21	AA54982	Human adenosine re	c 186	36	3.3	39	24	ABK27885	Oligonucleotide fr
110	37	3.4	31	21	AA54982	Human C/EBP polyu	c 187	35.5	3.2	26	15	AAQ79219	Guanosine rich oli
111	37	3.4	31	21	AA54982	Human adenosine re	c 188	35.5	3.2	26	18	AAQ79219	Viral integrase in
112	37	3.4	31	22	AA54982	Human single nucle	c 189	35.5	3.2	26	19	AAQ79226	Oligonucleotide #1
113	37	3.4	31	22	AA54982	Human single nucle	c 190	35.5	3.2	27	18	AAQ79226	Viral integrase in
114	37	3.4	32	18	AAQ85354	Spider silk protei	c 191	35.5	3.2	27	19	AAQ79221	Oligonucleotide #1
115	37	3.4	33	22	AAQ85354	Human IL-17RH2 hyb	c 192	35.5	3.2	27	22	AAH46002	Synthetic oligonuc
116	37	3.4	34	24	AAQ85354	Chimeric RGS prote	c 193	35.5	3.2	27	22	AAH46002	Synthetic oligonuc
117	37	3.4	35	24	AAQ85354	Cricetulus griseus	c 194	35.5	3.2	33	24	ABL50723	Human protease act
118	37	3.4	35	14	AAQ36248	HIV4par, directed	c 195	35.5	3.2	33	24	ABL50723	PAR PCR primer SEQ
119	37	3.4	38	11	AAQ04981	Sequence binding t	c 196	35	3.2	19	20	AAQ206700	PCR primer DLX3E3F
120	37	3.4	38	13	AAQ33257	Triplex forming ol	c 197	35	3.2	21	24	ABN85560	Bcl-2 related olig
121	37	3.4	38	15	AAQ33257	Sequence of synth	c 198	35	3.2	21	24	ABN85560	SNP specific lower
122	37	3.4	38	15	AAQ33257	Sequence of contro	c 199	35	3.2	23	22	AAH39814	Oligonucleotide SP
123	37	3.4	38	15	AAQ33257	Sequence of synth	c 200	35	3.2	23	22	AAH39814	Human zinc-finger
124	37	3.4	38	15	AAQ33257	Triple helix-formi	c 201	35	3.2	24	22	AAH44526	Oligonucleotide us
125	37	3.4	38	15	AAQ33257	Triple helix-formi	c 202	35	3.2	25	20	AAQ40789	Human GMMLP-1 25-m
126	37	3.4	38	15	AAQ33257	Guanosine rich oli	c 203	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
127	37	3.4	38	15	AAQ33257	Viral integrase in	c 204	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
128	37	3.4	38	15	AAQ33257	Oligonucleotide #3	c 205	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
129	37	3.4	40	17	AAQ33257	BCG deletion regio	c 206	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
130	37	3.4	40	20	AAQ33257	Circular plasmid e	c 207	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
131	37	3.4	40	21	AAQ33257	Polynucleotide seq	c 208	35	3.2	25	24	ABN04473	Human GMMLP-1 25-m
132	37	3.4	40	24	AAQ33257	Oligonucleotide 33	c 209	35	3.2	25	24	ABN04480	Human GMMLP-1 25-m
133	37	3.4	40	24	AAQ33257	Probe hybridising	c 210	35	3.2	26	16	AAQ89046	VEGF 2'-NH2-RNA nu
134	36	3.3	19	21	AAQ33257	Synthetic RNA sequ	c 211	35	3.2	26	20	AAQ40779	Genomic sequence s
135	36	3.3	20	20	AAQ33257	Antisense oligonuc	c 212	35	3.2	26	20	AAQ40779	Oligonucleotide us
136	36	3.3	20	21	AAQ33257	Antisense oligonuc	c 213	35	3.2	26	21	AAA26251	Bcl-2 antisense ol

c 214	35	3.2	26	22	AA75967	Rat Bcl-XL mutagen	287	3.1	24	24	ABI86275	Capture oligonucle
c 215	35	3.2	27	21	AAZ50048	5' PCR primer-2 fo	288	3.1	25	21	RAC95580	HLA DOB gene PCR p
c 216	35	3.2	28	22	AAH44825	PCR primer specific	289	3.1	25	21	RAC95582	HLA DOB gene PCR p
c 217	35	3.2	30	16	AAQ89019	VSGF 2'-NH2-RNA nu	290	3.1	25	21	RAC95629	HLA DOB gene PCR p
c 218	35	3.2	30	18	AAQ98807	Primer 63-6 for G	291	3.1	25	21	AAQ95634	Human KTM1a porti
c 219	35	3.2	30	20	AAZ25334	Human chemokine al	292	3.1	25	24	ABQ64648	Human KTM1a porti
c 220	35	3.2	30	20	AAZ25337	Human chemokine al	293	3.1	25	24	ABQ64649	c-fos antisense ol
c 221	35	3.2	30	21	AAZ35231	PCR primer RV-C us	294	3.1	28	16	AAQ83382	Reverse primer use
c 222	35	3.2	30	22	AAZ35231	PCR primer RV-C us	295	3.1	29	20	AAQ83382	Reverse primer use
c 223	35	3.2	30	24	ABK49835	Chromobacterium SC	296	3.1	29	20	AAQ83382	Reverse primer use
c 224	35	3.2	31	20	AAZ38868	Human ADAMTS prote	297	3.1	29	21	AAQ3828	Polymorphic fragme
c 225	35	3.2	31	20	AAZ38868	Human genomic DNA	298	3.1	29	21	AAQ3828	Polymorphic fragme
c 226	35	3.2	31	20	AAZ38868	Human genomic DNA	299	3.1	30	13	AAQ32894	Human apolipoprote
c 227	35	3.2	31	22	AAZ12735	Human biallelic po	300	3.1	30	17	AAQ32894	Human apolipoprote
c 228	35	3.2	31	22	AAZ12735	Human biallelic po	301	3.1	30	19	AAQ32894	Human apolipoprote
c 229	35	3.2	32	15	AAQ68918	zebrafish BMP2 cDN	302	3.1	30	19	AAQ32894	Human apolipoprote
c 230	35	3.2	33	18	AAQ68918	Oligo for CT elem	303	3.1	30	20	AAQ32894	Human apolipoprote
c 231	35	3.2	33	18	AAQ68918	Mouse bcl-w gene p	304	3.1	30	20	AAQ32894	Human apolipoprote
c 232	35	3.2	35	21	AAZ92083	PCR primer for GBP	305	3.1	31	13	AAQ32894	Human apolipoprote
c 233	35	3.2	36	14	AAQ44238	ICAM-1 cDNA revers	306	3.1	31	19	AAQ32894	Human apolipoprote
c 234	35	3.2	36	16	AAQ80032	5' flanking primer	307	3.1	31	19	AAQ32894	Human apolipoprote
c 235	35	3.2	36	18	AAQ80032	Human extracellular	308	3.1	31	21	AAQ32894	Human apolipoprote
c 236	35	3.2	36	20	AAQ80032	Hepatocyte growth	309	3.1	31	22	AAQ32894	Human apolipoprote
c 237	35	3.2	36	20	AAQ80032	PCR primer used to	310	3.1	31	22	AAQ32894	Human apolipoprote
c 238	35	3.2	37	15	AAQ87361	GM-CSF-IgG1-FC dir	311	3.1	31	22	AAQ32894	Human apolipoprote
c 239	35	3.2	37	20	AAQ59193	PCR primer choilpc	312	3.1	31	22	AAQ32894	Human apolipoprote
c 240	35	3.2	37	20	AAQ59193	Human antibody V-k	313	3.1	31	22	AAQ32894	Human apolipoprote
c 241	35	3.2	37	22	AAH24960	PCR primer FL15405	314	3.1	31	22	AAQ32894	Human apolipoprote
c 242	35	3.2	37	24	ABN89483	PCR primer for hum	315	3.1	32	20	AAQ32894	Human apolipoprote
c 243	35	3.2	37	24	ABK81251	Human obese gene p	316	3.1	32	20	AAQ32894	Human apolipoprote
c 244	35	3.2	37	24	AAQ32894	Polyimmunoglobulin	317	3.1	32	20	AAQ32894	Human apolipoprote
c 245	35	3.2	37	24	AAQ32894	Human chorionic go	318	3.1	32	20	AAQ32894	Human apolipoprote
c 246	35	3.2	38	21	AAQ32894	Oligonucleotide seq	319	3.1	32	20	AAQ32894	Human apolipoprote
c 247	35	3.2	39	21	AAQ32894	Arabidopsis GABA r	320	3.1	32	20	AAQ32894	Human apolipoprote
c 248	35	3.2	39	21	AAQ32894	Clostridium botuli	321	3.1	32	20	AAQ32894	Human apolipoprote
c 249	35	3.2	39	21	AAQ32894	PCR primer for cDN	322	3.1	32	20	AAQ32894	Human apolipoprote
c 250	35	3.2	40	21	AAQ32894	Human IL4Ralpha ge	323	3.1	32	20	AAQ32894	Human apolipoprote
c 251	35	3.1	37	22	AAQ32894	Polymerase chain re	324	3.1	32	20	AAQ32894	Human apolipoprote
c 252	35	3.1	40	21	AAQ32894	Primer taq82R. Sy	325	3.1	32	20	AAQ32894	Human apolipoprote
c 253	35	3.1	17	24	ABL31028	Polymerase chain re	326	3.1	32	20	AAQ32894	Human apolipoprote
c 254	35	3.1	17	24	ABL31028	Human HLA genotypi	327	3.1	32	20	AAQ32894	Human apolipoprote
c 255	35	3.1	18	15	AAQ77633	Human HLA genotypi	328	3.1	32	20	AAQ32894	Human apolipoprote
c 256	35	3.1	18	15	AAQ77633	Ribonucleotide to	329	3.1	32	20	AAQ32894	Human apolipoprote
c 257	35	3.1	18	15	AAQ77633	Antisense polynuc	330	3.1	32	20	AAQ32894	Human apolipoprote
c 258	35	3.1	18	15	AAQ77633	Antisense ribonuc	331	3.1	32	20	AAQ32894	Human apolipoprote
c 259	35	3.1	18	15	AAQ77633	Polymerase chain re	332	3.1	32	20	AAQ32894	Human apolipoprote
c 260	35	3.1	18	21	AAQ77633	Human bcl genes an	333	3.1	32	20	AAQ32894	Human apolipoprote
c 261	35	3.1	19	14	AAQ51960	Human HLA genotypi	334	3.1	32	20	AAQ32894	Human apolipoprote
c 262	35	3.1	19	14	AAQ51960	BCL-2 mRNA ribozym	335	3.1	32	20	AAQ32894	Human apolipoprote
c 263	35	3.1	19	22	AAQ57095	PKCalpha primer-pa	336	3.1	32	20	AAQ32894	Human apolipoprote
c 264	35	3.1	20	19	AAQ57095	Human Notch3 mutan	337	3.1	32	20	AAQ32894	Human apolipoprote
c 265	35	3.1	20	21	AAZ46977	Bcl-XL mRNA specif	338	3.1	32	20	AAQ32894	Human apolipoprote
c 266	35	3.1	20	22	AAZ46977	Human bcl-x antise	339	3.1	32	20	AAQ32894	Human apolipoprote
c 267	35	3.1	21	15	AAQ77636	Human bcl-x antise	340	3.1	32	20	AAQ32894	Human apolipoprote
c 268	35	3.1	21	15	AAQ77636	Ribonucleotide to	341	3.1	32	20	AAQ32894	Human apolipoprote
c 269	35	3.1	21	15	AAQ77636	Ribonucleotide to	342	3.1	32	20	AAQ32894	Human apolipoprote
c 270	35	3.1	21	15	AAQ77636	Antisense polynuc	343	3.1	32	20	AAQ32894	Human apolipoprote
c 271	35	3.1	21	15	AAQ77636	Antisense polynuc	344	3.1	32	20	AAQ32894	Human apolipoprote
c 272	35	3.1	21	15	AAQ77636	Antisense ribonuc	345	3.1	32	20	AAQ32894	Human apolipoprote
c 273	35	3.1	21	15	AAQ77636	Antisense ribonuc	346	3.1	32	20	AAQ32894	Human apolipoprote
c 274	35	3.1	21	15	AAQ77636	Polymerase chain re	347	3.1	32	20	AAQ32894	Human apolipoprote
c 275	35	3.1	21	16	AAQ78936	Primer V-R1 for cl	348	3.1	32	20	AAQ32894	Human apolipoprote
c 276	35	3.1	21	21	AAQ66244	Dog genomic marker	349	3.1	32	20	AAQ32894	Human apolipoprote
c 277	35	3.1	22	14	AAQ51952	BCL-2 mRNA ribozym	350	3.1	32	20	AAQ32894	Human apolipoprote
c 278	35	3.1	22	18	AAQ48499	Bax omega protein	351	3.1	32	20	AAQ32894	Human apolipoprote
c 279	35	3.1	24	15	AAQ77637	Ribonucleotide to	352	3.1	32	20	AAQ32894	Human apolipoprote
c 280	35	3.1	24	15	AAQ77637	Ribonucleotide to	353	3.1	32	20	AAQ32894	Human apolipoprote
c 281	35	3.1	24	15	AAQ77637	Antisense polynuc	354	3.1	32	20	AAQ32894	Human apolipoprote
c 282	35	3.1	24	15	AAQ77637	Antisense polynuc	355	3.1	32	20	AAQ32894	Human apolipoprote
c 283	35	3.1	24	15	AAQ77637	Antisense ribonuc	356	3.1	32	20	AAQ32894	Human apolipoprote
c 284	35	3.1	24	15	AAQ77637	Antisense ribonuc	357	3.1	32	20	AAQ32894	Human apolipoprote
c 285	35	3.1	24	15	AAQ77637	Polymerase chain re	358	3.1	32	20	AAQ32894	Human apolipoprote
c 286	35	3.1	24	15	AAQ77637	Polymerase chain re	359	3.1	32	20	AAQ32894	Human apolipoprote

C 360	34	3.1	40	21	AAZ96094	Polynucleotide seq	C 433	33	3.0	25	24	ABN13265	Human GDMPL-1 25-m
C 361	34	3.1	40	21	AAZ96115	Polynucleotide seq	C 434	33	3.0	25	24	ABN13266	Human GDMPL-1 25-m
C 362	34	3.1	40	21	AAZ37327	Human c-kit fragme	C 435	33	3.0	26	18	AAU70143	Primer pr 887 for
C 363	33.5	3.0	33	18	AAU85186	Equine rhinovirus	C 436	33	3.0	26	19	AAV56729	Human microsatelli
C 364	33.5	3.0	33	18	AAU85186	SFI-H3 PCR primer	C 437	33	3.0	26	22	AAV89906	Probe used to iden
C 365	33.5	3.0	36	21	AAQ99063	Cathepsin B substr	C 438	33	3.0	26	23	AAH78691	Mouse procollagen
C 366	33.5	3.0	36	21	AAU12882	DNA encoding cathe	C 439	33	3.0	26	24	ABQ88539	Human GPCR probe
C 367	33.5	3.0	36	21	AAZ30328	PCR primer 5' VLB5R	C 440	33	3.0	27	9	AAH82286	Probe for DNA enco
C 368	33.5	3.0	39	19	AAV21265	Tissue plasminogen	C 441	33	3.0	27	15	AAQ79234	Guanosine rich oli
C 369	33.5	3.0	40	21	AAU63513	Thyroid hormone re	C 442	33	3.0	27	17	AAU79233	GD domain region f
C 370	33.5	3.0	40	21	AAU63513	Human thyroid horm	C 443	33	3.0	27	17	AAU79233	Viral integrase in
C 371	33	3.0	40	22	AAU57145	Guanosine rich oli	C 444	33	3.0	27	18	AAU51652	Oligonucleotide #2
C 372	33	3.0	16	18	AAU79248	Viral integrase in	C 445	33	3.0	27	19	AAU79236	Saccharomyces cere
C 373	33	3.0	16	18	AAU51678	Viral integrase in	C 446	33	3.0	27	20	AAU27120	Human CDC28-#3 RNA
C 374	33	3.0	16	18	AAU51665	Viral integrase in	C 447	33	3.0	27	20	AAU00491	Human inflammatory
C 375	33	3.0	16	18	AAU79247	Oligonucleotide #4	C 448	33	3.0	27	22	AAH91288	Human CCR5
C 376	33	3.0	17	15	AAU79246	Guanosine rich oli	C 449	33	3.0	27	24	ABQ87922	Enterohaemorrhagic
C 377	33	3.0	17	15	AAU79233	Guanosine rich oli	C 450	33	3.0	27	24	ABQ87930	Enterohaemorrhagic
C 378	33	3.0	17	18	AAU51693	Viral integrase in	C 451	33	3.0	27	24	ABQ11182	DNA encoding Bax G
C 379	33	3.0	17	18	AAU51677	Viral integrase in	C 452	33	3.0	28	20	AAU09964	Mouse whey acidic
C 380	33	3.0	17	18	AAU51689	Viral integrase in	C 453	33	3.0	28	20	AAU55170	Bradykinin recepto
C 381	33	3.0	17	18	AAU51663	Viral integrase in	C 454	33	3.0	28	20	AAU55159	Bradykinin recepto
C 382	33	3.0	17	18	AAU51651	Viral integrase in	C 455	33	3.0	28	21	AAU20739	Human bradykinin r
C 383	33	3.0	17	19	AAU79268	Oligonucleotide #6	C 456	33	3.0	28	21	AAU0941	Mutagenic primer f
C 384	33	3.0	17	19	AAU79270	Oligonucleotide #6	C 457	33	3.0	28	21	AAU34617	Human adenosine re
C 385	33	3.0	17	19	AAU79208	Oligonucleotide #1	C 458	33	3.0	28	24	ABU49737	Human adenosine re
C 386	33	3.0	17	19	AAU79235	Oligonucleotide #2	C 459	33	3.0	28	24	ABU49737	pAM330 mutagenic p
C 387	33	3.0	17	19	AAU79245	Oligonucleotide #3	C 460	33	3.0	29	18	AAU22586	PCR primer #7 to i
C 388	33	3.0	17	19	AAU79256	Oligonucleotide #4	C 461	33	3.0	29	18	AAU22586	Human foetal liver
C 389	33	3.0	17	19	AAU79257	Oligonucleotide #5	C 462	33	3.0	29	21	AAU2450	Type C lectin PCR
C 390	33	3.0	17	19	AAU28225	Antisense oligonuc	C 463	33	3.0	29	21	AAU28236	Human alpha-2CAR n
C 391	33	3.0	17	20	AAU23633	Deletion sequence	C 464	33	3.0	30	16	AAU3284	Family 2 bFGF 2'-N
C 392	33	3.0	17	20	AAU18754	Target HIV antisense	C 465	33	3.0	30	16	AAU2630	Chromosome 11 (loc
C 393	33	3.0	17	20	AAU49365	HIV targetted anti	C 466	33	3.0	30	19	AAU37601	L. seeligeri 3327
C 394	33	3.0	18	15	AAU79203	Guanosine rich oli	C 467	33	3.0	30	20	AAU76188	Human Slit-1 PCR p
C 395	33	3.0	18	15	AAU79231	Guanosine rich oli	C 468	33	3.0	30	21	AAU99880	Reverse primer pr
C 396	33	3.0	18	15	AAU79232	Guanosine rich oli	C 469	33	3.0	30	21	AAU98253	P. oleovirans phac
C 397	33	3.0	18	16	AAU54754	Mouse IL-5 hamme	C 470	33	3.0	30	21	AAU98261	Z. ramigera phbc g
C 398	33	3.0	18	18	AAU51649	Viral integrase in	C 471	33	3.0	30	22	AAU56946	FIV-141 proviral g
C 399	33	3.0	18	18	AAU51650	Viral integrase in	C 472	33	3.0	30	22	AAU70665	2'NH2 RNA ligand t
C 400	33	3.0	18	18	AAU51621	Viral integrase in	C 473	33	3.0	30	23	ABU53307	Oligonucleotide li
C 401	33	3.0	18	19	AAU79212	Oligonucleotide #5	C 474	33	3.0	30	24	ABU91892	Mouse Diff6 PCR pr
C 402	33	3.0	18	19	AAU79231	Oligonucleotide #2	C 475	33	3.0	30	24	ABU12581	Blue light recepto
C 403	33	3.0	20	19	AAU41288	Antisense oligo MA	C 476	33	3.0	31	15	AAU74330	Human Igg-1 light
C 404	33	3.0	20	19	AAU56438	Mouse vWF PCR reve	C 477	33	3.0	31	16	AAU76237	Primer for amplifi
C 405	33	3.0	20	21	AAU65049	Human bcl genes an	C 478	33	3.0	31	18	AAU05354	PCR primer used to
C 406	33	3.0	20	21	AAU65049	Antisense oligonuc	C 479	33	3.0	31	18	AAU97361	Construction of pl
C 407	33	3.0	20	22	AAU44820	Human chromosome 1	C 480	33	3.0	31	19	AAU36712	Nucleotide sequenc
C 408	33	3.0	21	16	AAU43896	Recombinant C. his	C 481	33	3.0	31	20	AAU38848	Human genomic DNA
C 409	33	3.0	21	16	AAU43896	Recombinant C. his	C 482	33	3.0	31	20	AAU99479	PCR primer and pro
C 410	33	3.0	21	17	AAU35037	Triplex-forming ol	C 483	33	3.0	31	20	AAU68129	Oligonucleotide us
C 411	33	3.0	21	21	AAU59809	Primer for Bcl-X n	C 484	33	3.0	31	22	AAU30234	Human single nucle
C 412	33	3.0	21	22	AAU41791	Bcl-X gene PCR pri	C 485	33	3.0	31	22	AAU30998	Human single nucle
C 413	33	3.0	21	22	AAU96909	Human gene single	C 486	33	3.0	31	22	AAU97241	Human Chk1 ribozym
C 414	33	3.0	21	22	AAU96909	Human cytochrome P	C 487	33	3.0	31	22	AAU43465	CDNA clone HP03564
C 415	33	3.0	22	18	AAU63192	FSH receptor fshr	C 488	33	3.0	31	23	ABU97861	Non-endogenous hum
C 416	33	3.0	23	14	AAU48964	HepG2 histidyl trn	C 489	33	3.0	31	23	ABU97862	Non-endogenous hum
C 417	33	3.0	23	18	AAU89668	Human histidyl-trn	C 490	33	3.0	31	24	ABU67729	Novel transglutami
C 418	33	3.0	24	21	AAU95425	Cat flea HMT ligan	C 491	33	3.0	31	24	ABU67736	Novel transglutami
C 419	33	3.0	24	24	ABU04772	F-cassette structu	C 492	33	3.0	31	24	AAU17784	Human Igg1 light c
C 420	33	3.0	25	21	AAU36647	PCR primer VDE119	C 493	33	3.0	32	18	AAU90919	Primer for Von Hip
C 421	33	3.0	25	22	AAU38031	SNP specific SNPE	C 494	33	3.0	32	18	AAU94902	Reverse primer for
C 422	33	3.0	25	24	ABU64651	Human KTM1a porti	C 495	33	3.0	32	19	AAU18034	PrMADS2 promoter r
C 423	33	3.0	25	24	ABU64652	Human KTM1a porti	C 496	33	3.0	32	20	AAU38066	RGH nucleic acid g
C 424	33	3.0	25	24	ABU64654	Human KTM1a porti	C 497	33	3.0	32	20	AAU38066	Retrovirus RGH gag
C 425	33	3.0	25	24	ABU64655	Human KTM1a porti	C 498	33	3.0	32	22	AAU19089	Retrovirus RGH gag
C 426	33	3.0	25	24	ABU03934	Human GDMPL-1 25-m	C 499	33	3.0	32	22	AAU19099	HERV-H/RGH retrovi
C 427	33	3.0	25	24	ABU03935	Human GDMPL-1 25-m	C 500	33	3.0	32	22	AAU76874	Mouse mas-like (ML
C 428	33	3.0	25	24	ABU04421	Human GDMPL-1 25-m							PCR primer OGR38 f
C 429	33	3.0	25	24	ABU04422	Human GDMPL-1 25-m							
C 430	33	3.0	25	24	ABU13262	Human GDMPL-1 25-m							
C 431	33	3.0	25	24	ABU13263	Human GDMPL-1 25-m							
C 432	33	3.0	25	24	ABU13264	Human GDMPL-1 25-m							

ALIGNMENTS

RESULT 1

AAQ51961  
ID AAQ51961 standard; RNA; 36 BP.  
XX  
AC AAQ51961;  
XX  
DT 26-MAY-1994 (first entry)  
XX  
DE BCL-2 mRNA ribozyme cleavable nucleotide (1997).  
XX  
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.  
XX  
PS Homo sapiens.  
XX  
PN WO9323057-A.  
XX  
PD 25-NOV-1993.  
XX  
PF 13-MAY-1993; 93WO-US04573.  
XX  
PR 14-MAY-1992; 92US-0882822.  
PR 14-MAY-1992; 92US-0882885.  
PR 26-AUG-1992; 92US-0936110.  
PR 26-AUG-1992; 92US-0936421.  
PR 26-AUG-1992; 92US-0936422.  
PR 26-AUG-1992; 92US-0936531.  
PR 26-AUG-1992; 92US-0936532.  
PR 07-DEC-1992; 92US-0987131.  
PR 19-JAN-1993; 93US-0006122.  
PR 19-JAN-1993; 93US-0008910.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Draper KG, Thompson JD;  
XX  
DR WPT; 1993-386203/48.  
XX  
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA  
PT associated with tumours or mRNA expressed from gene encoding  
PT multiple drug resistance  
XX  
PS Claim 3; Fig 6; 69pp; English.  
XX  
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
CC associated with development or maintenance of chronic myelogenous  
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or  
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute  
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma  
CC and lung cancer. The full length mRNAs containing these target  
CC sequences, encode aberrant cellular proteins which are able to control  
CC cellular proliferation and are directly linked to a leukemic  
CC phenotype. These target sequences are identified by the ribozyme of  
CC the invention. The ribozymes is formed in a hammerhead motif, but may  
CC also be formed in the motif of a hairpin, hepatitis delta virus, group  
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit  
CC the development or expression of a transformed phenotype in man and  
CC other animals by modulating expression of the corresponding gene.  
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed  
CC cells elicits inhibition of the transformed state. Multiple drug  
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of  
CC drug resistance used by transformed cells and thus enhances drug  
CC therapies for tumours. The ribozymes may also be used to study  
CC genetic drift and mutations within cells.  
XX  
SQ Sequence 36 BP; 10 A; 13 C; 8 G; 5 U; 0 other;  
XX  
Alignment Scores:

Pred. No.: 1.59e+03 Length: 36  
Score: 66.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.98% Indels: 0  
DB: 14 Gaps: 0  
US-09-375-514-22 (1-205) x AAQ51961 (1-36)  
QY 181 LeuAanArgHisLeuHisthrTrpIleGlnAsp 191  
Db 3 CUGAACCGGCACCGCACCGUGGAUCCAGGAU 35  
RESULT 2  
AAQ51951  
ID AAQ51951 standard; RNA; 33 BP.  
XX  
AC AAQ51951;  
XX  
DT 26-MAY-1994 (first entry)  
XX  
DE BCL-2 mRNA ribozyme cleavable nucleotide (1592).  
XX  
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9323057-A.  
XX  
PD 25-NOV-1993.  
XX  
PF 13-MAY-1993; 93WO-US04573.  
XX  
PR 14-MAY-1992; 92US-0882822.  
PR 14-MAY-1992; 92US-0882885.  
PR 26-AUG-1992; 92US-0936110.  
PR 26-AUG-1992; 92US-0936421.  
PR 26-AUG-1992; 92US-0936422.  
PR 26-AUG-1992; 92US-0936531.  
PR 26-AUG-1992; 92US-0936532.  
PR 07-DEC-1992; 92US-0987131.  
PR 19-JAN-1993; 93US-0006122.  
PR 19-JAN-1993; 93US-0008910.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Draper KG, Thompson JD;  
XX  
DR WPT; 1993-386203/48.  
XX  
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA  
PT associated with tumours or mRNA expressed from gene encoding  
PT multiple drug resistance  
XX  
PS Claim 3; Fig 6; 69pp; English.  
XX  
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
CC associated with development or maintenance of chronic myelogenous  
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or  
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute  
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma  
CC and lung cancer. The full length mRNAs containing these target  
CC sequences, encode aberrant cellular proteins which are able to control  
CC cellular proliferation and are directly linked to a leukemic  
CC phenotype. These target sequences are identified by the ribozyme of  
CC the invention. The ribozymes is formed in a hammerhead motif, but may

CC also be formed in the motif of a hairpin, hepatitis delta virus, group  
 CC I intron or RNasep-like RNA. These ribozymes may be used to inhibit  
 CC the development or expression of a transformed phenotype in man and  
 CC other animals by modulating expression of the corresponding gene.  
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed  
 CC cells elicits inhibition of the transformed state. Multiple drug  
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of  
 CC drug resistance used by transformed cells and thus enhances drug  
 CC therapies for tumours. The ribozymes may also be used to study  
 CC genetic drift and mutations within cells.

XX SQ Sequence 33 BP; 5 A; 16 C; 7 G; 5 U; 0 other;

Alignment Scores:  
 Pred. No.: 5.79e+03 Length: 33  
 Score: 57.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 5.16% Indels: 0  
 DB: 14 Gaps: 0

US-09-375-514-22 (1-205) x AAQ51951 (1-33)

Qy 46 ProGlyIlePheSerSerGlnProGlyHis 55

Db 3 CCGGGCAUCUUCUCCGCCAGCCGGGCAC 32

RESULT 3

AAV28336/C

ID AAV28336 standard; cDNA; 24 BP.

XX AC AAV28336;

XX DT 02-OCT-1998 (first entry)

XX DE Rat bcl-y downstream primer.

XX ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat;

XX PCR; primer; amplification.

XX OS Synthetic.

XX OS Rattus sp.

XX US5789201-A.

XX PD 04-AUG-1998.

XX PF 11-FEB-1997; 97US-0798897.

XX PR 23-FEB-1996; 96US-0012201.

XX PR 11-FEB-1997; 97US-0798897.

XX (COCE-) COCENSYS INC.

XX Guastella J;

XX WPI; 1998-446079/38.

XX Nucleic acids encoding B-cell lymphoma-y protein - useful for  
 PT producing recombinant protein for use in treating uncontrolled cell  
 PT growth e.g. cancers

XX Example; Column 11; 27pp; English.

XX The primers AAV28335 and AAV28336 were used to amplify the rat bcl-y  
 CC gene. The mammalian bcl-y genes encode a protein that is a member of the  
 CC bcl-2 family, components in the cell death pathway. The bcl-2 family  
 CC have both apoptotic activity and the apoptosis blocking activity. bcl-y  
 CC falls in the apoptosis activity category. The recombinant protein may  
 CC be used to prevent uncontrolled cell growth, either by its direct  
 CC administration to recombinant genetic constructs to increase its  
 CC expression in vivo. Also, antisense constructs can be used in disorders  
 CC where prevention of cell death is desired.

XX SQ Sequence 24 BP; 3 A; 9 C; 1 G; 5 T; 6 other;

Alignment Scores:  
 Pred. No.: 5.66e+03 Length: 24  
 Score: 55.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.98% Indels: 0  
 DB: 19 Gaps: 0

US-09-375-514-22 (1-205) x AAV28336 (1-24)

Qy 188 TrpIleGlnAspAnGlyGlyTrp 195

Db 24 TGGATCCARGAYAAAYGGNGTGG 1

RESULT 4

AAV15948/C

ID AAV15948 standard; DNA; 24 BP.

XX AC AAV15948;

XX DT 20-MAY-1999 (first entry)

XX DE PCR primer used to amplify cDNA encoding the rat bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
 KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
 KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
 KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
 KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
 KW premature cell death; cell death stimulator; prolonged cell life span;  
 KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
 KW parasite; PCR primer; ss.

XX OS Synthetic.

XX OS Rattus sp.

XX US5883229-A.

XX PD 16-MAR-1999.

XX PF 25-NOV-1997; 97US-0978523.

XX PR 23-FEB-1996; 96US-0012201.

XX PR 11-FEB-1997; 97US-0798897.

XX PR 25-NOV-1997; 97US-0978523.

XX PA (COCE-) COCENSYS INC.

XX PI Guastella J;

XX WPI; 1999-214150/18.

XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
 PT for modulating programmed cell death

XX Example 1; Columns 11; 26pp; English.

XX PCR primers AAV15947-48 were used to amplify cDNA encoding rat bcl-y  
 CC protein (Rbcl-y). The specification also describes human bcl-y protein  
 CC (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought  
 CC to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y  
 CC and Hbcl-y proteins may be used to treat conditions associated with a  
 CC disruption of the cell death pathway. If they act as cell death  
 CC inhibitors, they may be used in therapies to treat subjects suffering  
 CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
 CC degenerative diseases (especially multiple sclerosis), myocardial  
 CC infarction, vitally induced cell death, aging, spinal cord injuries and  
 CC amyotrophic lateral sclerosis- conditions where cells under go premature  
 CC cell death as a result of triggers which may or may not be apparent.  
 CC They may also be used in this way to develop cell lines which remain

CC viable in culture for an extended period. In contrast, if they act as  
 CC cell death stimulators, Bcl-2 and Bcl-xL may be used to treat conditions  
 CC associated with prolonged cell life span such as cancer (especially  
 CC Kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may  
 CC also be used to cause cell death in, and hence control, parasites.

XX Sequence 24 BP; 3 A; 9 C; 1 G; 5 T; 6 other;

#### Alignment Scores:

Pred. No.: 24  
 Score: 5.66e+03 Length: 24  
 Matches: 8  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.98% Indels: 0  
 DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAI15948 (1-24)

YY 188 TptleGlnAspAsnGlyGlyTrp 195

DB 24 TGGATCARGAYATGGGNGTGG 1

#### RESULT 5

AAI64676/c

ID AAI64676 standard; DNA; 33 BP.

AC AAI64676;

DT 04-DEC-2001 (first entry)

DE Human proteolytic enzyme regulatory protein 12 PCR primer 3.

KW Human; proteolytic enzyme regulatory protein 12; cytostatic; virucidal;  
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour; HIV;  
 KW infection; human immunodeficiency virus; immunological disease;  
 KW PCR primer; ss.

OS Homo sapiens.

PN WO200172793-A1.

PD 04-OCT-2001.

PF 26-MAR-2001; 2001WO-CN00476.

PR 28-MAR-2000; 2000CN-0115200.

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

PI Mao Y, Xie Y;

DR WPI; 2001-597100/67.

XX New human proteolytic enzyme regulatory protein 12 and encoded  
 PT polynucleotide, applicable in diagnosis and treatment of cancer,  
 PT haemopathy, human immunodeficiency virus infection, immunological  
 PT diseases and inflammation

PS Example 4; Page 16; 34pp; Chinese.

XX The invention relates to human proteolytic enzyme regulatory protein 12  
 CC with cytostatic, virucidal, immunomodulatory, antiinflammatory and  
 CC haemostatic activity. The polypeptide and encoded polynucleotide are  
 CC applicable in diagnosis and treatment of malignant tumour, haemopathy,  
 CC HIV infection, immunological diseases and various inflammations. The  
 CC present sequence is that of a human proteolytic enzyme regulatory protein  
 CC 12 PCR primer, useful to the invention.

XX Sequence 33 BP; 8 A; 5 C; 7 G; 13 T; 0 other;

#### Alignment Scores:

Pred. No.: 1.69e+04 Length: 33  
 Score: 50.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 4.53% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAI64676 (1-33)

QY 181 LeuAsnArgHisLeuHisThrTrpIle 189

DB 31 TTAAATAGGCATACACACATGGATC 5

#### RESULT 6

AAH45307

ID AAH45307 standard; DNA; 36 BP.

XX AAH45307;

AC AAH45307;

DT 10-SEP-2001 (first entry)

XX Human Bcl-2 PCR primer oligo-10.

KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; PCR primer; ss.

OS Homo sapiens.

PN WO200142459-A1.

PD 14-JUN-2001.

PF 07-DEC-2000; 2000WO-JP08667.

PR 09-DEC-1999; 99JP-0350427.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Shibasaki F, Kuma H;

DR WPI; 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related  
 PT disorders

PS Example 1; Page 39; 43pp; Japanese.

XX The invention relates to an apoptosis inhibitor comprising the  
 CC amino acid sequence of Bcl-2 protein in which at least one serine  
 CC residue is substituted by alanine or aspartic acid. The protein has  
 CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence was used to  
 CC amplify DNA encoding the human Bcl-2 protein.

SQ Sequence 36 BP; 7 A; 10 C; 15 G; 4 T; 0 other;

#### Alignment Scores:

Pred. No.: 1.85e+04 Length: 36  
 Score: 50.00 Matches: 9  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.53% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45307 (1-36)

QY 1 MetAlaHisAlaGlyArgThrGlyTyr 9

DB 10 ATGGCGCACGCTGGGAGAACGGGTAC 36

#### RESULT 7

ABN85362/c

ID ABN85362 standard; DNA; 24 BP.

XX ABN85362;

AC ABN85362;

XX 07-OCT-2002 (first entry)  
XX Bcl-2 related oligonucleotide #3.  
XX Interferon; cytokine; alpha-1 interferon; beta-1 interferon; Bcl-2;  
XX gamma-1 interferon; interferon-regulated enzyme; ds-protein kinase;  
XX 2',5'-oligoadenylatesynthetase; RNAase L; Fas antigen;  
XX gamma-actin cytoskeleton protein; ss.  
XX Unidentified.  
XX RU2181773-C2.  
XX 27-APR-2002.  
XX 16-MAR-2000; 2000RU-0106253.  
XX 16-MAR-2000; 2000RU-0106253.  
XX (AMVI-) A MED VIROLOGY RES INST.  
XX Sokolova TM, Uryvaev LV;  
XX WPI; 2002-391288/42.  
XX Method of assay of human cytokine status at genetic level  
XX Claim 1; Page 7; 10pp; Russian.  
XX The present invention relates to a method for estimating transcription  
XX levels of genes encoding interferons, interferon-dependent and  
XX proliferative cytokines. The method involves determining cytokine mRNA  
XX levels, using a combination of RT-PCR with blot- and dot-hybridisation.  
XX To illustrate the method, cytokines (alpha-1, beta-1 and gamma-1  
XX interferon), interferon-regulated enzymes  
XX (2',5'-oligoadenylatesynthetase, RNAase L and ds-protein kinase) and  
XX factors of cellular proliferation (Bcl-2, Fas antigen and gamma-actin  
XX cytoskeleton protein) were used. The present oligonucleotide was used to  
XX illustrate the invention.  
XX Sequence 24 BP; 2 A; 15 C; 2 G; 5 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 1.42e+04 Length: 24  
Score: 49.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.44% Indels: 0  
DB: 24 Gaps: 0  
US-09-375-514-22 (1-205) x ABN85362 (1-24)  
QY 139 ArgAspGlyValAsnTrpGlyArg 146  
Db 24 AGGACGGGGTGAACCTGGGGAGG 1  
RESULT 8  
ABN85361/C  
ID ABN85361 standard; DNA; 21 BP.  
XX AC ABN85361;  
XX 07-OCT-2002 (first entry)  
XX Bcl-2 related oligonucleotide #2.  
XX Interferon; cytokine; alpha-1 interferon; beta-1 interferon; Bcl-2;  
XX gamma-1 interferon; interferon-regulated enzyme; ds-protein kinase;  
XX 2',5'-oligoadenylatesynthetase; RNAase L; Fas antigen;  
XX gamma-actin cytoskeleton protein; ss.  
XX Unidentified.

XX RU2181773-C2.  
XX 27-APR-2002.  
XX 16-MAR-2000; 2000RU-0106253.  
XX 16-MAR-2000; 2000RU-0106253.  
XX (AMVI-) A MED VIROLOGY RES INST.  
XX Sokolova TM, Uryvaev LV;  
XX WPI; 2002-391288/42.  
XX Method of assay of human cytokine status at genetic level  
XX Claim 1; Page 7; 10pp; Russian.  
XX The present invention relates to a method for estimating transcription  
XX levels of genes encoding interferons, interferon-dependent and  
XX proliferative cytokines. The method involves determining cytokine mRNA  
XX levels, using a combination of RT-PCR with blot- and dot-hybridisation.  
XX To illustrate the method, cytokines (alpha-1, beta-1 and gamma-1  
XX interferon), interferon-regulated enzymes  
XX (2',5'-oligoadenylatesynthetase, RNAase L and ds-protein kinase) and  
XX factors of cellular proliferation (Bcl-2, Fas antigen and gamma-actin  
XX cytoskeleton protein) were used. The present oligonucleotide was used to  
XX illustrate the invention.  
XX Sequence 21 BP; 2 A; 5 C; 9 G; 5 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 1.68e+04 Length: 21  
Score: 47.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 4.26% Indels: 0  
DB: 24 Gaps: 0  
US-09-375-514-22 (1-205) x ABN85361 (1-21)  
QY 182 AsnArgHisLeuHisThrTrr 188  
Db 21 AACCGGCACCTGCACACCTGG 1  
RESULT 9  
AAQ86646  
ID AAQ86646 standard; DNA; 33 BP.  
XX AC AAQ86646;  
XX 27-SEP-1995 (first entry)  
XX Bcl-2 splice donor site.  
XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
XX leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;  
XX ss.  
XX Synthetic.  
XX WO9508350-A.  
XX 30-MAR-1995.  
XX 20-SEP-1994; 94WO-US10725.  
XX 20-SEP-1993; 93US-0124256.  
XX (REED/) REED J C.  
XX Reed JC;  
PI



XX WPI; 1995-139394/18.  
 XX  
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment  
 PT of human solid tumours, esp. breast cancer  
 XX  
 XX Disclosure; Page 13; 108pp; English.  
 XX  
 CC The antisense oligonucleotide SD-AS (AAQ86645) is complementary to a  
 CC portion of the splice donor site of the pre-mRNA coding strand of the  
 CC human bcl-2 gene. It reduces the expression of bcl-2 gene product,  
 CC thereby inducing programmed cell death of certain cancer cells. The  
 CC corresp. bcl-2 sense splice donor site region was synthesized for use  
 CC as a control.  
 XX  
 XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 2.68e+04 Length: 33  
 Score: 47.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.26% Indels: 0  
 DB: 16 Gaps: 0

US-09-375-514-22 (1-205) x AAQ86646 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200  
 ID AAV19654 standard; DNA; 33 BP.  
 AC AAV19654;  
 XX  
 DT 12-JUN-1998 (first entry)  
 DE Human bcl-2 oligonucleotide 2.  
 XX  
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;  
 KW cancer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5734033-A.  
 XX  
 PD 31-MAR-1998.  
 XX  
 PF 24-MAR-1994; 94US-0288692.  
 XX  
 PR 21-FEB-1992; 92US-0840716.  
 PR 22-DEC-1988; 88US-0288692.  
 PR 24-MAR-1994; 94US-0217082.  
 XX  
 XX (UIPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Reed J;  
 XX  
 DR WPI; 1998-229881/20.  
 XX  
 PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful  
 PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)  
 XX  
 XX Disclosure; Columns 3-4; 21pp; English.  
 XX  
 CC This is a human bcl-2 oligonucleotide based on which an antisense  
 CC oligonucleotide complementary to the splice donor site of the human  
 CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle  
 CC strategic sites such as the translation initiation site, donor and  
 CC acceptor splicing sites, or sites for transportation or degradation.

CC Blocking translation at such strategic sites prevents the formation of a  
 CC functional bcl-2 gene product. These oligonucleotides may be used for  
 CC treating cancers associated with high levels of bcl-2 gene expression,  
 CC especially lymphomas and some leukaemias.  
 XX  
 XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 2.68e+04 Length: 33  
 Score: 47.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.26% Indels: 0  
 DB: 19 Gaps: 0

US-09-375-514-22 (1-205) x AAV19654 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200  
 ID AAV19654 standard; DNA; 33 BP.  
 AC AAV19654;  
 XX  
 DT 12-JUL-2002 (first entry)  
 DE Bcl-2 antisense oligonucleotide.  
 XX  
 KW B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;  
 KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
 KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
 KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
 KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
 KW head and neck cancer; brain cancer; cytostatic; human; gene therapy;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200217852-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 23-AUG-2001; 2001WO-US26414.  
 XX  
 PR 25-AUG-2000; 2000US-227970P.  
 PR 29-SEP-2000; 2000US-237009P.  
 PR 10-NOV-2000; 2000US-0709170.  
 XX  
 XX (GENT-) GENTA INC.  
 XX  
 XX Warrel RP, Klem RE, Fingert H;  
 XX  
 DR WPI; 2002-371796/40.  
 XX  
 XX Treating or preventing cancer, tumors and carcinomas, comprises  
 XX administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
 XX high doses for short period for time with one or more cancer  
 XX therapeutics -  
 XX  
 PS Disclosure; Page 53; 64pp; English.  
 XX  
 CC The present sequence is that of a B cell lymphoma/leukaemia-2  
 CC (bcl-2) antisense oligonucleotide. The present invention is  
 CC directed to the use of bcl-2 antisense oligomers, particularly  
 CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.  
 CC Administration at high doses results in significant therapeutic  
 CC responses, including low toxicity, high tolerance and prolonged  
 CC survival. Administration at high doses for short periods of time  
 CC (less than 14 days) also provides significant therapeutic responses  
 CC in the treatment of cancer. The bcl-2 antisense oligomer may also

CC be used to increase the sensitivity of a subject to cancer  
 CC therapeutics, and in combination with hormone treatment or gene  
 CC therapy. Conditions that may be treated or prevented include  
 CC cancer of the haematopoietic system, skin, bone and soft tissue,  
 CC reproductive system, genitourinary system, breast, endocrine  
 CC system, brain, central nervous system, peripheral nervous system,  
 CC kidney, lung, respiratory system, thorax, gastrointestinal and  
 CC alimentary canal, lymph nodes, pancreas, hepatobiliary system, or  
 CC cancer of unknown primary site, non-Hodgkin's lymphoma, Hodgkin's  
 CC lymphoma, leukaemia, colon carcinoma, rectal carcinoma, pancreatic,  
 CC breast, ovarian, prostate, cervical, testicular, head and neck or  
 CC brain cancer, renal cell carcinoma, hepatoma, bile duct carcinoma,  
 CC choriocarcinoma, lung carcinoma, bladder carcinoma and melanoma  
 CC (all claimed).

SQ Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Alignment Scores:  
 Pred. No.: 2.68e+04 Length: 33  
 Score: 47.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.26% Indels: 0  
 DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABL54152 (1-33)

QY 193 GlyGlyTrpValGlyAlaSerGly 200

DB 10 GGAGCGTGGGTAGGTGCATCTGGT 33

RESULT 12

AAQ51954

ID AAQ51954 standard; RNA; 28 BP.

AC AAQ51954;

DT 26-MAY-1994 (first entry)

DE BCL-2 mRNA ribozyme cleavable nucleotide (1729).

Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
 resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
 actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
 adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
 human; chronic myelogenous leukemia; CML; follicular lymphoma;  
 B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
 neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
 hairpin; hepatitis delta virus; group I intron; RNaseP; ss.

Homo sapiens.

WO9323057-A.

25-NOV-1993.

13-MAY-1993; 93WO-US04573.

14-MAY-1992; 92US-0882822.

14-MAY-1992; 92US-0882885.

26-AUG-1992; 92US-0936110.

26-AUG-1992; 92US-0936421.

26-AUG-1992; 92US-0936422.

26-AUG-1992; 92US-0936531.

26-AUG-1992; 92US-0936532.

07-DEC-1992; 92US-0987131.

19-JAN-1993; 93US-0006122.

19-JAN-1993; 93US-0008910.

(RIBO-) RIBOZYME PHARM INC.

Draper KG, Thompson JD;

DR WPI; 1993-386203/48.

XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA  
 PT associated with tumours or mRNA expressed from gene encoding  
 PT multiple drug resistance

XX Claim 3; Fig 6; 69pp; English.

XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
 CC associated with development or maintenance of chronic myelogenous  
 CC leukemia (CML); promyelocytic leukemia, Burkitt's lymphoma, or  
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute  
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma  
 CC and lung cancer. The full length mRNAs containing these target  
 CC sequences, encode aberrant cellular proteins which are able to control  
 CC cellular proliferation and are directly linked to a leukemic  
 CC phenotype. These target sequences are identified by the ribozyme of  
 CC the invention. The ribozymes are formed in a hammerhead motif, but may  
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group  
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit  
 CC the development or expression of a transformed phenotype in man and  
 CC other animals by modulating expression of the corresponding gene.  
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed  
 CC cells elicits inhibition of the transformed state. Multiple drug  
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of  
 CC drug resistance used by transformed cells and thus enhances drug  
 CC therapies for tumours. The ribozymes may also be used to study  
 CC genetic drift and mutations within cells.

SQ Sequence 28 BP; 3 A; 13 C; 7 G; 5 U; 0 other;

Alignment Scores:

Pred. No.: 3.08e+04 Length: 28  
 Score: 45.00 Matches: 9  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 4.08% Indels: 0  
 DB: 14 Gaps: 0

US-09-375-514-22 (1-205) x AAQ51954 (1-28)

QY 91 ProValValHisLeuAlaLeuArgGln 99

DB 1 CCUGUGUGUCCACCGUGCCGCCGCCCAA 27

RESULT 13

AAAT36054/C

ID AAT36054 standard; DNA; 24 BP.

XX AAT36054;

AC AAT36054;

XX 20-NOV-1996 (first entry)

XX bcl-2 reverse PCR primer.

DE Cardiovascular disease; differential expression; target gene;

XX pathway gene; fingerprint gene; atherosclerosis; ischaemia;

KW reperfusion; hypertension; restenosis; arterial inflammation;

KW vector; antibody; diagnosis; gene therapy; drug screening;

XX bcl-2; polymerase chain reaction; PCR; primer; ss.

OS Synthetic.

XX WO9624604-A1.

PN 15-AUG-1996.

XX 09-FEB-1996; 96WO-US01883.

XX 07-JUN-1995; 95US-0485573.

XX 10-FEB-1995; 95US-0386844.

XX (MILL-) MILLENNIUM PHARM INC.

XX Falb DA;  
 PI WPI; 1996-384391/38.  
 XX  
 XX New genes differentially expressed in cardiovascular disease - and  
 PT related vectors, host cells, proteins and antibodies, for diagnosis,  
 PT monitoring, treatment and drug screening  
 XX  
 XX Example 7; Page 12; 200pp; English.  
 PS  
 XX Monocyte RNA from apolipoprotein E (apoE)-deficient and control  
 CC mice was compared using primers for mouse bcl-2 (AAT36053 and  
 CC AAT36054) and gamma-actin (AAT36055 and AAT36056). bcl-2 mRNA  
 CC levels were significantly lower in the apoE-deficient mice (an  
 CC animal model of atherosclerosis). Regulation of the mouse bcl-2  
 CC gene appeared to be regulated by serum cholesterol levels.  
 CC Similar results were obtained with the human bcl-2 and glutathione  
 CC peroxidase genes (see also AAT36057-58). The discovery that certain  
 CC genes (see also AAT26029-36) are differentially expressed in  
 CC cardiovascular diseases can be used to develop methods for the  
 CC diagnosis and treatment of such diseases.  
 XX  
 XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3.06e+04 Length: 24  
 Score: 44.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.99% Indels: 0  
 DB: 17 Gaps: 0  
 US-09-375-514-22 (1-205) x AAT36054 (1-24)  
 QY 140 AspGlyValAsnTrpGlyArg 146  
 Db 23 GATGGGTGAACCTGGGGGAGG 3  
 RESULT 14  
 AAX26250/c  
 ID AAX26250 standard; DNA; 24 BP.  
 XX  
 AC AAX26250;  
 XX  
 XX 24-MAY-1999 (first entry)  
 DT  
 XX Reverse primer for RT-PCR analysis of mouse bcl-2 mRNA.  
 DE  
 XX Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
 KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
 KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
 KW RT-PCR; primer; bcl-2; mouse; ss.  
 XX  
 XX Synthetic.  
 OS Mus sp.  
 XX  
 XX US5882925-A.  
 PN  
 XX 16-MAR-1999.  
 PD  
 XX  
 XX 09-FEB-1996; 96US-0599654.  
 PF  
 XX 09-FEB-1996; 96US-0599654.  
 PR  
 XX 10-FEB-1995; 95US-0386844.  
 PR  
 XX 07-JUN-1995; 95US-0485573.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Falb DA;  
 PI  
 XX WPI; 1999-214071/18.  
 XX

PT New polynucleotides consisting of residues 1-1929 of the rchd502  
 PT gene - are differentially expressed in cardiovascular disease  
 PT states, and can therefore be used to treat and diagnose  
 PT cardiovascular diseases  
 XX  
 XX Disclosure; Column 9; 121pp; English.  
 PS  
 XX The invention relates to a rchd502 target/fingerprint gene encoding a  
 CC transmembrane protein. The invention provides cDNAs contained in plasmids  
 CC pFCHD502SF (ATCC 6981) and pFCHD502SJ (ATCC 6982) that encode the  
 CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
 CC disease states. Cultured genetically engineered host cell containing the  
 CC rchd502 polynucleotides in operative association with a nucleotide  
 CC regulatory element are used for producing a polypeptide rchd502 gene  
 CC product. Identifying that the fingerprint/target gene rchd502 is  
 CC differentially expressed (up-regulated) by endothelial cells subjected  
 CC to shear stress, provides a tool for the diagnosis and treatment of  
 CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
 CC hypertension, restenosis. The fingerprint gene is useful for testing the  
 CC efficacy of candidate drugs in basic research and in clinical trials and  
 CC or imaging of a diseased cardiovascular tissue. The gene may also be  
 CC used in screening for ligands of target gene product receptor domains, as  
 CC well as antagonists of the ligand-receptor interaction.  
 XX  
 XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3.06e+04 Length: 24  
 Score: 44.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.99% Indels: 0  
 DB: 20 Gaps: 0  
 US-09-375-514-22 (1-205) x AAX26250 (1-24)  
 QY 140 AspGlyValAsnTrpGlyArg 146  
 Db 23 GATGGGTGAACCTGGGGGAGG 3  
 RESULT 15  
 AAV81830/c  
 ID AAV81830 standard; DNA; 24 BP.  
 XX  
 AC AAV81830;  
 XX  
 XX 11-MAR-1999 (first entry)  
 DT  
 XX Mouse bcl-2 reverse primer #1.  
 DE  
 XX Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
 KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;  
 KW primer; ss.  
 XX  
 XX Synthetic.  
 OS Mus sp.  
 XX  
 XX US5849578-A.  
 PN  
 XX 15-DEC-1998.  
 PD  
 XX  
 XX 15-MAR-1996; 96US-0616844.  
 PF  
 XX 09-FEB-1996; 96US-0599654.  
 PR  
 XX 10-FEB-1995; 95US-0386844.  
 PR  
 XX 07-JUN-1995; 95US-0458873.  
 PR  
 XX 15-MAR-1996; 96US-0616844.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Falb DA;  
 PI  
 XX WPI; 1999-069743/06.  
 XX

XX DNA encoding rchd528 polypeptide - associated with cardiovascular  
PT disease  
XX  
XX Example; Column 95; 122pp; English.  
XX  
XX The present invention describes rchd528 protein. A method has been  
CC developed for producing the rchd528 gene product. The present invention  
CC also describes methods and compositions for the treatment and diagnosis  
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
CC present sequence represents a primer used in an example from the present  
CC invention.  
XX  
XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 3.06e+04 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 20 Gaps: 0  
US-09-375-514-22 (1-205) x AAV81830 (1-24)  
Qy 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGGAGG 3  
RESULT 16  
AA88587/C  
ID AA88587 standard; DNA; 24 BP.  
XX  
XX AA88587;  
XX  
XX 05-FEB-2001 (first entry)  
XX  
XX PCR primer for mouse bcl-2 gene.  
XX  
XX Mouse; bcl-2 gene; differential expression; atherosclerosis;  
KW cardiovascular disease; diagnosis; therapy; PCR primer; ss.  
KW  
XX Mus sp.  
XX  
XX US6124433-A.  
XX  
XX 26-SEP-2000.  
XX  
XX 06-OCT-1997; 97US-0944496.  
XX  
XX 09-FEB-1996; 96US-0599654.  
PR 10-FEB-1995; 95US-0386844.  
PR 07-JUN-1995; 95US-0485573.  
XX  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Gimbrone MA, Falb DA;  
XX  
XX WPI; 2000-611017/58.  
XX  
XX Novel isolated rchd502 polypeptides, differentially expressed in  
PT response to endothelial cell shear stress, used for diagnosis,  
PT monitoring clinical trails, and treating cardiovascular diseases such  
XX as ischemia -  
XX  
XX Example 7; Column 9; 123pp; English.  
XX  
XX This oligonucleotide is a reverse PCR primer for the mouse bcl-2  
CC gene. It was used with the forward primer given in AAA88586 in a  
CC quantitative RT-PCR analysis of mouse bcl-2 mRNA levels in  
CC apoE-deficient mice, a murine model of atherosclerosis. bcl-2

CC mRNAs were shown to be lower in apoE-deficient mice relative to  
CC wild-type controls. The invention provides novel human genes (see  
CC AAA88576-83) that are differentially expressed in cardiovascular  
CC disease states, and which are of diagnostic and therapeutic use.  
XX  
XX Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 3.06e+04 Length: 24  
Score: 44.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.99% Indels: 0  
DB: 21 Gaps: 0  
US-09-375-514-22 (1-205) x AAA88587 (1-24)  
Qy 140 AspGlyValAsnTrpGlyArg 146  
Db 23 GATGGGTGAACCTGGGGGAGG 3  
RESULT 17  
AAZ89800/C  
ID AAZ89800 standard; cDNA; 24 BP.  
XX  
XX AAZ89800;  
XX  
XX 05-MAY-2000 (first entry)  
XX  
XX Reverse primer for mouse bcl2 amplification.  
XX  
XX Differentially expressed; cardiovascular disease; atherosclerosis;  
KW ischaemia; reperfusion; hypertension; restenosis; arterial inflammation;  
KW bcl2; differential display analysis; ss.  
XX  
XX Mus sp.  
XX  
XX US6020463-A.  
XX  
XX 01-FEB-2000.  
XX  
XX 06-OCT-1997; 97US-0944423.  
XX  
XX 09-FEB-1996; 96US-0599654.  
PR 10-FEB-1995; 95US-0386844.  
PR 07-JUN-1995; 95US-0485573.  
XX  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Gimbrone MA, Falb DA;  
XX  
XX WPI; 2000-146911/13.  
XX  
XX Marker proteins for the diagnosis of cardiovascular diseases such as  
PT atherosclerosis and hypertension, comprising peptide sequences derived  
PT from the rchd523 transmembrane protein -  
XX  
XX Disclosure; Column 9; 121pp; English.  
XX  
XX This sequence represents a PCR primer used to amplify the mouse bcl2  
CC nucleotide sequence. The primer is used in methods for the  
CC identification of the marker proteins and differentially expressed genes  
CC of the invention. The invention relates to the rchd523 transmembrane  
CC polypeptide (see AAY78506) encoded by cDNA contained in the plasmid  
CC pfchd523. The rchd523 protein is differentially expressed in diseased  
CC cells compared to healthy cells. The rchd523 protein may be used as a  
CC marker protein for the diagnosis of cardiovascular diseases including  
CC atherosclerosis, ischaemia, reperfusion, hypertension, restenosis and  
CC arterial inflammation. rchd523 peptides may be used as antigens in the  
CC production of antibodies specific for rchd523. The anti-rchd523  
CC antibodies may then be used in diagnostic assays to quantitate rchd523  
CC peptides in samples.

XX SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:  
Pred. No.: 24  
Score: 3.06e+04  
Length: 44.00  
Matches: 7  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.99%  
Indels: 0  
DB: 21  
Gaps: 0

US-09-375-514-22 (1-205) x AAZ89800 (1-24)

QY 140 AspGlyValAsnTrrpGlyArg 146

DB 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 18

AAZ88011/c

ID AAZ88011 standard; DNA; 24 BP.

XX AC AAZ88011;

DT 19-APR-2000 (first entry)

DE Mouse bcl-2 reverse PCR primer SEQ ID NO:11.

KW Cardiovascular disease; diagnosis; atherosclerosis; ischaemia;  
KW reperfusion; hypertension; restenosis; arterial inflammation;  
KW antiarteriosclerotic; vasotropic; hypotensive; PCR primer; ss.

XX OS Mus sp.

XX US6018025-A.

XX PD 25-JAN-2000.

XX PF 06-OCT-1997; 97US-0944868.

XX PR 09-FEB-1996; 96US-0599654.

XX PR 10-FEB-1995; 95US-0386844.

XX PR 07-JUN-1995; 95US-0485573.

XX PA (MILL-) MILLENIUM PHARM INC.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Falb DA, Gimbrone MA;

XX WPI; 2000-136704/12.

Isolated polypeptide for treating and diagnosing cardiovascular disease, such as, atherosclerosis, ischemia/reperfusion, hypertension, restenosis and arterial inflammation -

XX Example; Column 9; 122pp; English.

The present invention describes an isolated polypeptide (I) comprising either the amino acid sequence of 1481 residues, given in AA68447, or an amino acid sequence encoded by the cDNA contained in plasmids pRCHD528A (ATCC 69985), pRCHD528B (ATCC 69986) and pRCHD528C (ATCC 69987). The polypeptide is useful in the treatment and diagnosis of cardiovascular disease, such as, atherosclerosis, ischemia/reperfusion, hypertension, restenosis and arterial inflammation. AAZ88001 to AAZ88040, CC and AA68444 to AA68457 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 24 BP; 4 A; 14 C; 1 G; 5 T; 0 other;

Alignment Scores:  
Pred. No.: 24  
Score: 3.06e+04  
Length: 44.00  
Matches: 7  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0

XX SQ Query Match: 3.99% Indels: 0  
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAZ88011 (1-24)

QY 140 AspGlyValAsnTrrpGlyArg 146

DB 23 GATGGGTGAACCTGGGGGAGG 3

RESULT 19

AAZ73296

ID AAZ73296 standard; DNA; 25 BP.

XX AC AAZ73296;

DT 06-DEC-2000 (first entry)

DE Bcl-2 specific gene amplification PCR primer #1.

KW STAT; signal transducer and activator of transcription; human; cancer;  
KW cell signalling; cytokine; growth factor; oncogenesis; tumour;  
KW apoptosis; cytostatic; tumorigenesis; PCR primer; ss.

XX OS Homo sapiens.

XX WO200044774-A2.

XX PD 03-AUG-2000.

XX PF 27-JAN-2000; 2000WO-US01845.

XX PR 27-JAN-1999; 99US-0117600.

XX PA (UYSF-) UNIV SOUTH FLORIDA.

XX PI Jove R, Dalton W, Sebt S, Yu H, Heller R, Jaroszeski M;

XX WPI; 2000-505964/45.

XX Administering antagonists of STAT (signal transducer and activator of transcription) signaling in cells for the treatment of cancers -

XX Example 9; Page 31; 92pp; English.

The present invention describes methods for inhibiting the growth of (I), inducing apoptosis in (II), inhibiting tumorigenesis in (III), inhibiting neoplastic transformation in (IV) cancer cells and for enhancing the effectiveness of chemo-(IV) and radiotherapies (VI) for the treatment of cancer. The methods comprise administering an antagonist of STAT (signal transducer and activator of transcription) signalling. The methods may be used for inhibiting the growth of cancer cells (I), inducing apoptosis in cancer cells (II), inhibiting tumorigenesis in cancer cells (III), inhibiting neoplastic transformation in cancer cells (IV) and for enhancing the effectiveness of chemo-(IV) and radiotherapies (VI) for the treatment of cancer. The present sequence represents a specific gene amplification PCR primer for bcl-2, which is used in an example from the present invention.

XX SQ Sequence 25 BP; 3 A; 13 C; 5 G; 4 T; 0 other;

Alignment Scores:  
Pred. No.: 25  
Score: 3.19e+04  
Length: 44.00  
Matches: 8  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatch: 0  
Query Match: 3.99%  
Indels: 0  
DB: 21  
Gaps: 0

US-09-375-514-22 (1-205) x AAZ73296 (1-25)

QY 102 AspAspPheSerArgTyrArg 109

DB 2 GACGACTTCTCCGCCGCTACGCG 25

```

RESULT 20
AAH45305/c
ID AAH45305 standard; DNA; 27 BP.
XX
AC AAH45305;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human Bcl-2 mutagenic primer oligo-8 for S161A substitution.
XX
KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142459-A1.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-JP08667.
XX
PR 09-DEC-1999; 95JP-0350427.
XX
PA (HISM ) HISAMITSU PHARM CO LTD.
XX
PI Shibasaki F, Kuma H;
XX
DR WPI; 2001-381681/40.
XX
PT New apoptosis inhibitors, useful for treating apoptosis related
PT disorders -
XX
PS Example 1; Page 11; 43pp; Japanese.
XX
CC The invention relates to an apoptosis inhibitor comprising the
CC amino acid sequence of Bcl-2 protein in which at least one serine
CC residue is substituted by alanine or aspartic acid. The protein has
CC increased apoptosis inhibitory activity compared with the wild type
CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC of disorders caused by apoptosis. The present sequence was used to
CC create a mutant Bcl-2 protein of the invention.
XX
SQ Sequence 27 BP; 5 A; 12 C; 5 G; 5 T; 0 other;

Alignment Scores:
Pred. No.: 3.46e+04 Length: 27
Score: 44.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45305 (1-27)
QY 157 MetCysValGluSerValAsnArgGlu 165
Db 27 ATGTGTGTGGAGCGCGTCAACGGGAG 1

RESULT 21
AAL46663/c
ID AAL46663 standard; DNA; 27 BP.
XX
AC AAL46663;
XX
DT 05-AUG-2002 (first entry)
XX
DE Human bcl-2 mRNA probe.
XX
KW Human; bcl-2; cancer detection; disseminated cancer cell; cytostatic;
XX
PR probe; ss.
XX
OS Homo sapiens.

```

```

XX WO200237113-A2.
XX
PN 10-MAY-2002.
XX
PF 05-NOV-2001; 2001WO-EPI2786.
XX
PR 03-NOV-2000; 2000DE-1054635.
PR 03-NOV-2000; 2000US-245854P.
XX
PA (GIES/) GIESING M.
XX
PI Giesing M, Grill H, Boeckmann B, Suchy B;
XX
DR WPI; 2002-426739/45.
XX
PT Clinically validating target from disseminated cancer cells by
PT determining whether status of target determined in cancer cells of
PT individuals correlates with cancer-related information about clinical
PT status of individuals -
XX
PS Example 3; Page 55; 57pp; English.
XX
CC The present invention relates to a method for the clinical validation of
CC a target from disseminated cancer cells, characterised in that for a
CC population of individuals it is determined whether a status of the target
CC determined in disseminated cancer cells of the individuals correlates
CC with at least one cancer-related information about the clinical status of
CC the individuals. The method is useful for clinically validating target
CC from disseminated cancer cells. The present sequence is a probe used
CC to demonstrate the method of the invention.
XX
SQ Sequence 27 BP; 6 A; 7 C; 7 G; 7 T; 0 other;

Alignment Scores:
Pred. No.: 3.46e+04 Length: 27
Score: 44.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.99% Indels: 0
DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x AAL46663 (1-27)
QY 172 AsnIleAlaLeuTrpMetThrGlu 179
Db 25 AACATCGCCCTGTGGATGACTGAG 2

RESULT 22
ABK66508/c
ID ABK66508 standard; DNA; 25 BP.
XX
AC ABK66508;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #596.
XX
PR Primer; ss; DNA microarray; differential expression analysis; human.
XX
OS Homo sapiens.
XX
PN US6352829-B1.
XX
PD 05-MAR-2002.
XX
PF 05-JAN-1999; 99US-0225928.
XX
PR 21-MAY-1997; 97US-0859998.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Chenchik A, Jokhadze G, Bibilashvilli R;

```

XX WPI; 2002-314699/35.  
XX Producing sub-population of labeled nucleic acids, useful for analysing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers -  
XX  
XX Example 3; SEQ ID No 596; 11pp; English.  
XX  
XX The invention relates to producing a sub-population of labeled nucleic  
CC acids (NAs) comprising contacting a NA sample from a physiological  
CC source, with a pool of 50 distinct gene specific primers under suitable  
CC conditions to enzymatically generate sub-population of NAs, where  
CC each gene specific primer has a sequence complementary to a distinct  
CC mRNA, and each labeled NA is generated using a single gene specific  
CC primer. The method is useful for producing a sub-population of labeled  
CC NAs which is useful for analysing the differences in the RNA profiles  
CC between several different physiological sources, where the method  
CC comprises producing subpopulation of labeled NAs for the different  
CC physiological sources, comprising the populations for each physiological  
CC source to identify differences in the population, where the comparison  
CC is preferably performed by hybridising the labeled NAs for each of the  
CC distinct physiological sources to an array of probe NAs stably  
CC associated with the surface of a substrate to produce a hybridisation  
CC pattern for each of the sources, and comparing the patterns for each of  
CC the sources, where differential gene expression assays are  
CC utilised in differential expression analysis of diseased a normal  
CC tissue e.g. neoplastic a normal tissue, or different tissue or  
CC subissue types. The present sequence is a human gene specific PCR  
CC primer used in the method of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from USPTO at  
CC <http://wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1>.  
XX  
XX Sequence 25 BP; 5 A; 11 C; 4 G; 5 T; 0 other;  
SQ

Alignment Scores:  
Pred. No.: 4.34e+04 Length: 25  
Score: 42.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABK66508 (1-25)  
QY 189 IleGlnAspAsnGlyGlyTrpVal 196  
DB 24 ATCCAAGACCCAGGGTGGTGGGTG 1

RESULT 23  
AAH45298/C  
ID AAH45298 standard; DNA; 27 BP.  
XX  
XX AAH45298;  
XX 10-SEP-2001 (first entry)  
XX Human Bcl-2 mutagenic primer oligo-1 for S24A substitution.  
XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200142459-A1.  
XX 14-JUN-2001.  
XX 07-DEC-2000; 2000WO-JP08667.  
XX 09-DEC-1999; 99JP-0350427.  
XX The invention relates to an apoptosis inhibitor comprising the  
CC amino acid sequence of Bcl-2 protein in which at least one serine  
CC residue is substituted by alanine or aspartic acid. The protein has

XX (HISM ) HISAMITSU PHARM CO LTD.  
XX Shibazaki F, Kuma H;  
XX WPI; 2001-381681/40.  
XX  
XX New apoptosis inhibitors, useful for treating apoptosis related  
PT disorders -  
XX  
XX Example 1; Page 10; 43pp; Japanese.  
XX  
XX The invention relates to an apoptosis inhibitor comprising the  
CC amino acid sequence of Bcl-2 protein in which at least one serine  
CC residue is substituted by alanine or aspartic acid. The protein has  
CC increased apoptosis inhibitory activity compared with the wild type  
CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
CC of disorders caused by apoptosis. The present sequence was used to  
CC create a mutant Bcl-2 protein of the invention.  
XX  
XX Sequence 27 BP; 5 A; 7 C; 8 G; 7 T; 0 other;  
SQ

Alignment Scores:  
Pred. No.: 4.67e+04 Length: 27  
Score: 42.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 3.80% Indels: 0  
DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45298 (1-27)  
QY 20 HisTyrLysLeuSergGlnArgGlyTyr 28  
DB 27 CATTATAAGCTGGCGAGACCGGTAC 1

RESULT 24  
AAH45302/C  
ID AAH45302 standard; DNA; 27 BP.  
XX  
XX AAH45302;  
XX 10-SEP-2001 (first entry)  
XX Human Bcl-2 mutagenic primer oligo-5 for S116A substitution.  
XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200142459-A1.  
XX 14-JUN-2001.  
XX 07-DEC-2000; 2000WO-JP08667.  
XX 09-DEC-1999; 99JP-0350427.  
XX (HISM ) HISAMITSU PHARM CO LTD.  
XX Shibazaki F, Kuma H;  
XX WPI; 2001-381681/40.  
XX New apoptosis inhibitors, useful for treating apoptosis related  
PT disorders -  
XX  
XX Example 1; Page 11; 43pp; Japanese.  
XX  
XX The invention relates to an apoptosis inhibitor comprising the  
CC amino acid sequence of Bcl-2 protein in which at least one serine  
CC residue is substituted by alanine or aspartic acid. The protein has

CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence was used to  
 CC create a mutant Bcl-2 protein of the invention.

SQ Sequence 27 BP; 4 A; 8 C; 10 G; 5 T; 0 other;

Alignment Scores:  
 Pred. No.: 4.67e+04 Length: 27  
 Score: 42.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 88.88% Mismatches: 0  
 Query Match: 3.80% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45302 (1-27)

Qy 112 PheAlaGluMetSerGlnLeuHis 120  
 ID AAT42430 standard; DNA; 39 BP.  
 XX  
 AC AAT42430;  
 XX  
 DT 29-JUL-1997 (first entry)  
 XX  
 DE GD domain region for Bak encoding DNA, amino acid residues 82-94.  
 XX  
 KW Apoptosis; follicular lymphoma; tumour; p53; antibody; ss.  
 XX  
 OS Synthetic.  
 XX  
 PW WO9635951-A1.  
 XX  
 PD 14-NOV-1996.  
 XX  
 PF 06-MAY-1996; 96WO-US06122.  
 XX  
 PR 12-MAY-1995; 95US-0440391.  
 XX  
 PA (IMMU-) IMMUNOGEN INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 DR WPI; 1996-518805/51.  
 XX  
 PT P-PSDB; AAW06293.  
 XX

RESULT 25

AAT42430  
 ID AAT42430 standard; DNA; 39 BP.  
 XX  
 AC AAT42430;  
 XX  
 DT 29-JUL-1997 (first entry)  
 XX  
 DE GD domain region for Bak encoding DNA, amino acid residues 82-94.  
 XX  
 KW Apoptosis; follicular lymphoma; tumour; p53; antibody; ss.  
 XX  
 OS Synthetic.  
 XX  
 PW WO9635951-A1.  
 XX  
 PD 14-NOV-1996.  
 XX  
 PF 06-MAY-1996; 96WO-US06122.  
 XX  
 PR 12-MAY-1995; 95US-0440391.  
 XX  
 PA (IMMU-) IMMUNOGEN INC.  
 XX  
 PI Chittenden TD, Lutz RJ;  
 XX  
 DR WPI; 1996-518805/51.  
 XX  
 PT P-PSDB; AAW06293.  
 XX  
 PS Peptide(s) comprising GD domains - have similar activities to wild  
 XX type Bak, and cause cellular apoptosis for treatment of viral  
 XX infection  
 XX  
 XX Claim 6; Page 45; 69pp; English.  
 XX  
 XX The term GD domain refers to a protein domain first identified in  
 XX Bak and shown to be essential for the interaction of Bak with Bcl-x(L)  
 XX and for Bak's cell killing function; and to peptides and/or molecules  
 XX capable of mimicking its structure and/or function. The present sequence  
 XX encodes a GD domain corresponding to amino acid residues 82-94 of Bak.  
 XX An antibody raised against a GD domain may be used to screen a cDNA  
 XX expression library for clones comprising cDNA inserts encoding  
 XX immunoreactive proteins. Truncated GD domain peptides have been  
 XX shown to maintain the protein binding and cell killing function  
 XX exhibited by wild type Bak. These molecules may induce apoptosis in  
 XX tumour cell. These peptides act independently of p53 status. Bak or  
 XX GD domain mimetics that inhibit Bcl-2 may be selectively toxic to  
 XX certain tumours, e.g. follicular lymphoma, which depend on high levels  
 XX of Bcl-2 for their continued growth and survival. GD domain mimetics  
 XX may also be used for combating viral infections by causing apoptosis  
 XX of infected cells.

SQ Sequence 39 BP; 11 A; 11 C; 11 G; 6 T; 0 other;

Alignment Scores:  
 Pred. No.: 6.81e+04 Length: 39  
 Score: 42.00 Matches: 7  
 Percent Similarity: 75.00% Conservative: 2  
 Best Local Similarity: 58.33% Mismatches: 3  
 Query Match: 3.80% Indels: 0  
 DB: 17 Gaps: 0

US-09-375-514-22 (1-205) x AAT42430 (1-39)

Qy 101 GlyAspAspPheSerArgArgTyrArgGlyAspPhe 112  
 ID AAT42430 standard; DNA; 39 BP.  
 XX  
 AC AAT42430;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE DNA encoding Bak GD domain region #1 for modulating apoptosis.  
 XX  
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; ds.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..39  
 FT /\*tag= a  
 FT /partial  
 FT /product= "Bak GD domain region #1"  
 FT /note= "This sequence lacks both start and stop codons"

RESULT 26

ABK11179  
 ID ABK11179 standard; DNA; 39 BP.  
 XX  
 AC ABK11179;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE DNA encoding Bak GD domain region #1 for modulating apoptosis.  
 XX  
 KW GD domain; apoptosis; interaction with Bcl-XL; cell killing function;  
 KW bak; cell death regulatory molecule; autoimmune disease; cancer; ds.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..39  
 FT /\*tag= a  
 FT /partial  
 FT /product= "Bak GD domain region #1"  
 FT /note= "This sequence lacks both start and stop codons"

US6221615-B1.  
 24-APR-2001.  
 25-JAN-1999; 99US-0236385.  
 12-MAY-1995; 95US-0440391.  
 08-AUG-1997; 97US-0908597.  
 (APOP-) APOPTOSIS TECHNOLOGY INC.  
 Chittenden TD, Lutz RJ;  
 WPI; 2002-234950/29.  
 P-PSDB; AAU77876.

Identifying agents (e.g. modulators of apoptosis) capable of modulating  
 GD domain mediated heterodimerisation or homodimerisation comprises  
 carrying out a heterodimerisation or homodimerisation assay

Disclosure; Fig 8B; 37pp; English.

The present invention relates to novel peptides, designated GD domains,  
 which are capable of modulating apoptosis. The GD domains are essential  
 for Bak's interaction with Bcl-XL, and to Bak's cell killing function.  
 The GD domains mediate key protein/protein interactions with multiple  
 cell death regulatory molecules. Also described are methods of  
 identifying agonists or antagonists of GD domains. The methods are  
 useful for identifying agents capable of modulating GD domain mediated  
 heterodimerisation or homodimerisation. The methods are particularly  
 useful in drug screening and design, e.g. for identifying agents for  
 treating autoimmune disease or cancer, or for identifying modulators  
 of apoptosis. The present DNA sequence encodes a GD domain region.

SQ Sequence 39 BP; 11 A; 11 C; 11 G; 6 T; 0 other;



Alignment Scores:  
 Pred. No.: 6.81e+04 Length: 39  
 Score: 42.00 Matches: 7  
 Percent Similarity: 75.00% Conservative: 2  
 Best Local Similarity: 58.33% Mismatches: 3  
 Query Match: 3.80% Indels: 0  
 DB: 24 Gaps: 0

US-09-375-514-22 (1-205) x ABK11179 (1-39)

Qy 101 GlyAspPheSerArgArgTyrArgGlyAspPhe 112  
 ||||| :|||  
 Db 1 GGGGACGACATCAACCGACGCTATGACTCAGAGTTC 36

RESULT 27

AAH45293/c  
 ID AAH45299 standard; DNA; 27 BP.

XX AC

XX AC

XX 10-SEP-2001 (first entry)

DE Human Bcl-2 mutagenic primer oligo-2 for S24D substitution.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Shibazaki F., Kuma H;

XX WPI; 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related disorders

XX Example 1; Page 10; 43pp; Japanese.

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence was used to create a mutant Bcl-2 protein of the invention.

XX Sequence 27 BP; 5 A; 6 C; 8 G; 8 T; 0 other;

Alignment Scores:  
 Pred. No.: 5.44e+04 Length: 27  
 Score: 41.00 Matches: 7  
 Percent Similarity: 77.78% Conservative: 0  
 Best Local Similarity: 77.78% Mismatches: 2  
 Query Match: 3.71% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45299 (1-27)

Qy 20 HistTyrLysLeuSerGlnArgGlyTyr 28

Db 27 CATTATAAGCTGGACACGACCGGCTAC 1

RESULT 28

AAH45306/c

ID AAH45306 standard; DNA; 27 BP.

XX AC

XX AAH45306;

XX 10-SEP-2001 (first entry)

XX Human Bcl-2 mutagenic primer oligo-9 for S161D substitution.

XX Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200142459-A1.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-JP08667.

XX 09-DEC-1999; 99JP-0350427.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Shibazaki F., Kuma H;

XX WPI; 2001-381681/40.

XX New apoptosis inhibitors, useful for treating apoptosis related disorders

XX Example 1; Page 11; 43pp; Japanese.

CC The invention relates to an apoptosis inhibitor comprising the amino acid sequence of Bcl-2 protein in which at least one serine residue is substituted by alanine or aspartic acid. The protein has increased apoptosis inhibitory activity compared with the wild type Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment of disorders caused by apoptosis. The present sequence was used to create a mutant Bcl-2 protein of the invention.

XX Sequence 27 BP; 6 A; 12 C; 4 G; 5 T; 0 other;

Alignment Scores:  
 Pred. No.: 5.44e+04 Length: 27  
 Score: 41.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 3.71% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAH45306 (1-27)

Qy 157 MetCysValGluSerValAsnArgGlu 165

Db 27 ATGTGTGTGGAGTCTCAACCGGGAG 1

RESULT 29

AAH45306/c

ID AAH45306 standard; DNA; 31 BP.

XX AC

XX AAH45306;

XX 22-APR-1998 (first entry)

XX Mouse bcl-w gene PCR primer 2.

XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; PCR primer; ss.

XX Synthetic.

XX Mus sp.

XX Key Location/Qualifiers  
 FH modified\_base 14  
 FT /\*tag= a  
 FT /mod\_base= i  
 FT /note= "inosine"  
 FT modified\_base 17  
 FT /\*tag= b  
 FT /mod\_base= i  
 FT /note= "inosine"  
 FT modified\_base 20  
 FT /\*tag= c  
 FT /mod\_base= i  
 FT /note= "inosine"  
 XX W09735971-A1.  
 XX 02-OCT-1997.  
 XX 27-MAR-1997; 97WO-A000199.  
 XX 27-MAR-1996; 96AU-0008965.  
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX Adams JM, Cory S, Gibson LM, Holmgren SP;  
 XX WPI; 1997-489635/45.  
 XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
 XX or inhibit cell survival, e.g. for treatment of cancer and  
 XX degenerative diseases  
 XX Example 1; Page 30; 86pp; English.  
 XX AAT96580 and AAT96579 are PCR primers used to amplify a novel gene,  
 XX bcl-w, a member of the mouse bcl-2 gene family. This gene promotes cell  
 XX survival, so its modulation is useful in treatment of cancer or  
 XX auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's  
 XX disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,  
 XX human immunodeficiency virus infection or in cell transplants.  
 XX Up-regulation of the gene can also be used to modify cell lines cultured  
 XX in vivo, e.g. to develop new lines, to facilitate isolation of  
 XX hybridomas and to increase survival of primary explants during genetic  
 XX modification. It can be used to produce recombinant Bcl-w for therapy,  
 XX diagnosis, antibody production or screening of potential modulators.  
 XX Sequence 31 BP; 5 A; 10 C; 5 G; 7 T; 4 other;  
 Alignment Scores:  
 Pred. No.: 6.27e+04 Length: 31  
 Score: 41.00 Matches: 6  
 Percent Similarity: 75.00% Conservative: 0  
 Best Local Similarity: 75.00% Mismatches: 2  
 Query Match: 3.71% Indels: 0  
 DB: 18 Gaps: 0  
 US-09-375-514-22 (1-205) x AAT96580 (1-31)  
 QY 188 TrrileGlnAspAsnGlyClyTrp 195  
 Db 31 TGGATCCCAAGANMANGNGGCTGG 8  
 RESULT 30  
 AAT92245/C  
 ID AAT92245 standard; DNA; 36 BP.  
 XX AC AAT92245;  
 XX 19-JAN-1998 (first entry)  
 XX DE Mercuric ion reductase mera PCR mutagenesis primer 3'A.  
 XX

KW Metal ion resistance; mercuric ion reductase; mera; mercury;  
 KW toxic heavy metal; transgenic plant; mutagenic; bacterial;  
 XX transposon; Tn21; PCR; ss.  
 OS Synthetic.  
 OS Transposon Tn21.  
 XX US5668294-A.  
 XX 16-SEP-1997.  
 XX 21-APR-1995; 95US-0427097.  
 XX 21-APR-1995; 95US-0427097.  
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 XX Meagher RB, Summers AO;  
 XX WPI; 1997-470112/43.  
 XX DNA encoding mercuric ion reductase in plant-expressible form - for  
 XX producing transgenic plants resistant to toxic heavy metals  
 XX Example 1; Column 45; 52pp; English.  
 XX The present sequence represents a PCR mutagenesis primer used to  
 XX mutagenise the mera coding sequence derived from transposon Tn21, to  
 XX adapt it for plant expressibility. The nucleic acid molecule produced  
 XX is useful for producing transgenic plants that are resistant to toxic  
 XX heavy metals (especially mercury) and so can be used to remediate and/or  
 XX revegetate contaminated areas. The bacterial mera gene is derived from  
 XX the transposon Tn21, which was originally isolated from the  
 XX Incompatibility Group IncFII resistance plasmid NR1.  
 XX Sequence 36 BP; 8 A; 13 C; 9 G; 6 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.31e+04 Length: 36  
 Score: 41.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 3.71% Indels: 0  
 DB: 18 Gaps: 0  
 US-09-375-514-22 (1-205) x AAT92245 (1-36)  
 QY 75 ProAlaAlaProGlyAlaAlaAlaGly 83  
 Db 35 CCTGCTGCGCGGCTGAGGCTGCAGGA 9  
 RESULT 31  
 AAZ28595/C  
 ID AAZ28595 standard; DNA; 36 BP.  
 XX AC AAZ28595;  
 XX 24-DEC-1999 (first entry)  
 XX DE Primer 3'N for Tn21 mera gene.  
 XX Organometal; resistance; transcription; translation; regulation; mera;  
 KW transposon; Tn21; merB; mercuric ion reductase; organomercury lyase; ss;  
 KW transgenic plant; detoxification; metal compound; soil; sediment; primer;  
 KW aquatic environment; bioremediation; contamination; PCR; amplification.  
 OS Synthetic.  
 OS Transposon Tn21.  
 XX US5965796-A.  
 XX 12-OCT-1999.  
 XX





PR 23-OCT-1995; 95US-0535168.  
 PR 19-MAR-1996; 96US-0013688.  
 PR 25-MAR-1996; 96US-0014007.  
 PR 17-APR-1996; 96US-0015714.  
 XX (ARON-) ARONEX PHARM INC.  
 XX Pennewald S, Hogan ME, Mazumder A, Ojwang JO, Pommier Y;  
 PI Rando RF, Zengdegi JG;  
 XX WPI; 1997-132569/12.  
 XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit  
 PT viral enzyme responsible for integrating viral nucleic acid into the  
 PT host genome  
 XX  
 PS Claim 3; Page 141; 245pp; English.  
 XX AAT51619-T51698 are oligonucleotides used to inhibit the production  
 CC of viruses within a host cell. The oligonucleotides may form guanosine  
 CC tetrads (structures formed of eight hydrogen bonds by coordination of  
 CC the four oxygen atoms of guanine with alkali cations believed to bind  
 CC to the centre of a quadruplex, and by strong stacking interactions) and  
 CC are used to prevent the integration of viral nucleic acid into a host  
 CC genome. The oligonucleotides inhibit functioning of the integrase enzyme  
 CC and hence prevent viral infection. Viral infections that may be treated  
 CC include human immunodeficiency virus (HIV), Epstein Barr virus (EBV),  
 CC herpes simplex virus (HSV), human papilloma virus (HPV), adenovirus,  
 CC respiratory syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis  
 CC B virus (HBV), especially HIV-1 infection.  
 XX  
 SQ Sequence 38 BP; 0 A; 0 C; 29 G; 9 T; 0 other;  
 Alignment Scores: Length: 38  
 Pred. No.: 7.72e+04 Matches: 8  
 Score: 41.00 Conservative: 0  
 Percent Similarity: 50.00% Mismatches: 2  
 Best Local Similarity: 50.00% Indels: 6  
 Query Match: 3.71% Gaps: 1  
 DB: 18  
 US-09-375-514-22 (1-205) x AAT51620 (1-38)  
 Qy 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59  
 Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCCC 3  
 RESULT 36  
 AAX79211/c  
 ID AAX79211 standard; DNA; 38 BP.  
 XX  
 AC AAX79211;  
 XX  
 DT 31-AUG-1999 (first entry)  
 XX  
 DE Oligonucleotide #4 forms an intramolecular stacked tetrad structure.  
 XX  
 KW Column: box; stacked tetrad; inhibition; replication; pathophysiological;  
 KW herpes simplex virus; HSV; human papilloma virus; Epstein Barr Virus;  
 KW HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCMV;  
 KW respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;  
 KW human T-cell leukaemia virus; HTLV; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_site 1..38  
 FT /\*tag= a  
 FT /note= "optionally contains phosphodiester  
 FT internucleotide linkages"  
 FT  
 FT misc\_structure 1..38  
 FT /\*tag= b  
 FT /note= "forms intramolecular stacked tetrad or 3D

FT  
 XX  
 PN WO9833807-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 03-FEB-1998; 98WO-US01974.  
 XX  
 PR 09-DEC-1997; 97US-0987574.  
 PR 04-FEB-1997; 97US-0037374.  
 XX  
 XX (ARON-) ARONEX PHARM INC.  
 XX Cossum PA, Hogan ME, Ojwang JO, Rando RF, Wallace TL;  
 PI WPI; 1998-446809/38.  
 XX  
 XX New guanosine-rich tetrad forming oligonucleotide(s) - used for  
 PT inhibiting virus replication for treating e.g. herpes simplex,  
 PT papilloma, HIV, adenovirus or hepatitis B virus infection  
 XX  
 PS Disclosure; Page 135; 140pp; English.  
 XX  
 CC Sequences AAX79210-X79275 represent oligonucleotides (ON) which are able  
 CC to form a columnar box or "stacked tetrad" structure by intramolecular  
 CC internucleotide binding. The ONs are used to inhibit the replication  
 CC of viruses. They are able to suppress virus production for prolonged  
 CC periods after an initial short treatment regimen. They can be used for  
 CC treating pathophysiological states caused by viruses such as herpes  
 CC simplex virus, human papilloma virus, Epstein Barr virus, HIV,  
 CC adenovirus, respiratory syncytial virus, hepatitis B virus, human  
 CC cytomegalovirus and HTLV I and II.  
 XX  
 SQ Sequence 38 BP; 0 A; 0 C; 29 G; 9 T; 0 other;  
 Alignment Scores: Length: 38  
 Pred. No.: 7.72e+04 Matches: 8  
 Score: 41.00 Conservative: 0  
 Percent Similarity: 50.00% Mismatches: 2  
 Best Local Similarity: 50.00% Indels: 6  
 Query Match: 3.71% Gaps: 1  
 DB: 19  
 US-09-375-514-22 (1-205) x AAX79211 (1-38)  
 Qy 44 ProAlaProGlyIlePheSerSerGlnProGlyHisThrProHisPro 59  
 Db 32 CCCACCCCA-----CCCCCCCCACACCCACACCCC 3  
 RESULT 37  
 AAX79211/c  
 ID AAX79211 standard; DNA; 39 BP.  
 XX  
 AC AAX79211;  
 XX  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE Cdn primer Bclx 2-39.  
 XX  
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;  
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;  
 KW shock; lymphoma; eczema; primer; polymerase chain reaction; PCR;  
 KW ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 19  
 FT /\*tag= a  
 FT /mod\_base= i  
 FT modified\_base 22  
 FT /\*tag= b  
 FT /mod\_base= i

columnar box structure"

FT misc\_difference 25  
FT /tag= c  
FT /note= "base n at position 25 is not identified"  
FT misc\_difference 28  
FT /tag= d  
FT /note= "base n at position 28 is not identified"  
XX  
PN W09515084-A.  
XX  
XX 08-JUN-1995.  
XX  
XX 30-NOV-1994; 94WO-US13930.  
XX  
XX 07-OCT-1994; 94US-0320157.  
PR 30-NOV-1993; 93US-0160067.  
XX  
XX (LXRB-) LXR BIOTECHNOLOGY INC.  
XX  
XX Barr PJ, Kiefer MC;  
XX  
XX WPI; 1995-215106/28.  
XX  
XX New nucleic acid sequences encoding Cdn apoptosis modulators - and  
PT related vectors, transformed cells, proteins and antibodies, useful  
PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury  
PT etc.  
XX  
XX Disclosure; Fig.1; 66pp; English.  
XX  
XX In order to identify new Bcl-2 family members, degenerate PCR  
CC primers (AAQ95495-96) based on sequences in these regions were used  
CC in the amplification of human heart and B lymphoblastoid cell  
CC line WI-L2 cDNA. Cdn-1 cDNA (AAQ95492) was obtd.  
XX  
XX Sequence 39 BP; 7 A; 12 C; 5 G; 9 T; 6 other;  
SQ  
Alignment Scores:  
Pred. No.: 7.93e+04 Length: 39  
Score: 41.00 Matches: 6  
Percent Similarity: 75.00% Conservative: 0  
Best Local Similarity: 75.00% Mismatches: 2  
Query Match: 3.71% Indels: 0  
DB: 16 Gaps: 0  
US-09-375-514-22 (1-205) x AAQ95496 (1-39)  
Qy 188 TrpIleGlnAspAsnGlyGlyTrp 195  
Db 39 TGGATHCARGANGCANGGNGTGG 16  
RESULT 38  
ID ABK52487/C  
XX ID ABK52487 standard; DNA; 24 BP.  
XX AC ABK52487;  
XX  
XX 14-AUG-2002 (first entry)  
XX  
XX Fluorescent probe for DNA encoding human bcl-2.  
XX  
XX Human; detection of early stage allergic disease; atopic dermatitis;  
KW antiallergic; eosinocyte; eosinophil; bcl-2; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= labelled with FAM  
FT modified\_base 24  
FT /tag= b

FT /mod\_base= OTHER  
FT /note= "OTHER= labelled with TAMRA  
XX (6-carboxy-N,N,N',N'-tetramethylrhodamine)"  
PN JP2002119281-A.  
XX 23-APR-2002.  
XX  
XX 11-OCT-2000; 2000JP-0311193.  
XX  
XX 11-OCT-2000; 2000JP-0311193.  
XX  
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.  
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.  
XX  
XX WPI; 2002-475327/51.  
XX  
XX Detecting early stage allergic diseases with markers of 7 genes of  
PT GM-CSF R-beta, GM-CSF R-alpha, IL-3 R-alpha, PAF R, bcl-2, bcl-x and  
PT CD44 in eosinophils  
XX  
XX Example 1; Page 20; 25pp; Japanese.  
XX  
XX The present invention relates to a method for detecting early stage  
CC allergic diseases, particularly atopic dermatitis. The method  
CC comprises determining the expression levels of granulocyte macrophage  
CC colony stimulating factor receptor alpha or beta (GM-CSF R-alpha  
CC or -beta), interleukin 3 receptor alpha (IL-3 R-alpha), bcl-2,  
CC bcl-x, platelet activation factor receptor (PAF R) or CD44 in  
CC eosinocytes of a subject to be tested. The method further comprises  
CC comparison with expression levels in healthy volunteers. The method  
CC is useful for the early diagnosis and treatment of early stage  
CC allergic diseases such as atopic dermatitis. The present sequence  
CC represents a probe used in the methods of the present invention.  
XX  
XX Sequence 24 BP; 6 A; 11 C; 3 G; 4 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 5.62e+04 Length: 24  
Score: 40.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.62% Indels: 0  
DB: 24 Gaps: 0  
US-09-375-514-22 (1-205) x ABK52487 (1-24)  
Qy 143 AsnTrpGlyArgIleValala 149  
Db 22 AACTGGGGGAGGATGTGGCC 2  
RESULT 39  
ID AAT08792/C  
XX ID AAT08792 standard; DNA; 27 BP.  
XX AC AAT08792;  
XX  
XX 01-JUL-1996 (first entry)  
XX  
XX Cytokine production inhibitor J111-56.  
XX  
XX Cytokine; tumour necrosis factor-alpha; TNF-alpha; lipopolysaccharide;  
KW mitogen-induced; colinear triplex; capping group; cholesterol;  
XX tumour cell; glioblastoma cell; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 27  
FT /tag= a  
FT /note= "linked to cholesterol"  
XX  
XX W09532628-A1.  
PN



CC See also AAV13426-28 and AAR13939.

XX Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:  
Pred. No.: 9.47e+04 Length: 40  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 12 Gaps: 0

US-09-375-514-22 (1-205) x AAV13427 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGACGCCACATCCA 21

RESULT 42

AAV74159

ID AAV74159 standard; DNA; 40 BP.

XX AC AAV74159;

XX DT 12-APR-1999 (first entry)

XX DE Human mature von Willebrand Factor DNA probe.

XX KW von Willebrand Factor; vWF; human; GPIb binding domain;  
XX KW antiagregant; platelet aggregation; cerebrovascular disorder;  
XX KW cardiovascular disorder; myocardial infarction; angina;  
XX KW thrombolytic; platelet adhesion; therapy; probe; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5849702-A.

XX PD 15-DEC-1998.

XX PF 05-JUN-1995; 95US-0464962.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX PR 05-JUN-1995; 95US-0464962.

XX PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PI Garfinkel L, Richter T;

XX DR WPI; 1999-069781/06.

XX PT Composition for inhibiting blood platelet aggregation - containing

XX PS polypeptide comprising von Willebrand factor GPIb binding domain

XX Example 1; Column 12; 50pp; English.

XX CC This synthetic oligonucleotide corresponds to nucleotides  
XX CC flanking the 3' end of the human von Willebrand Factor (vWF) GPIb  
XX CC binding domain coding region. It was used as a probe for the  
XX CC detection of vWF sequences in a human endothelial cell cDNA  
XX CC library. A GPIb binding domain 5' probe was also used (see  
XX CC AAV74158). A series of vWF cDNA clones covering the entire GPIb  
XX CC binding domain (see AAV74157) were identified and isolated. The  
XX CC invention provides non-glycosylated, biologically active  
XX CC polypeptides (see AAV90119-20) which comprise the vWF GPIb binding  
XX CC domain. These are used in claimed methods for treating and  
XX CC preventing cerebrovascular and cardiovascular disorders, and for  
XX CC inhibiting platelet aggregation.

SQ Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:  
Pred. No.: 9.47e+04 Length: 40  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAV74159 (1-40)

QY 53 ProGlyHisThrProHisPro 59

DB 1 CCAGGACGACGCCACATCCA 21

RESULT 43

AAV08903

ID AAV08903 standard; DNA; 40 BP.

XX AC AAV08903;

XX DT 26-FEB-1999 (first entry)

XX DE Probe for Von Willebrand factor coding sequence.

XX KW Von Willebrand factor; GPIb binding domain; inhibitor; re-occlusion;  
XX KW platelet aggregation; cerebrovascular disorder; cardiovascular disorder;  
XX KW angioplasty; thrombi-containing platelet-rich aggregate; thrombosis;  
XX KW therapy; probe; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US5849536-A.

XX PD 15-DEC-1998.

XX PF 30-NOV-1994; 94US-0347594.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PI Garfinkel L, Richter T;

XX DR WPI; 1999-069733/06.

XX PT Polypeptide comprising von Willebrand factor GPIb binding domain -

XX PS useful as platelet aggregation inhibitor

XX Example 1; Column 13-14; 62pp; English.

XX CC This sequence represents a probe for DNA encoding the protein of the  
XX CC invention. The protein of the invention is the GPIb binding domain of the  
XX CC von Willebrand factor. The protein is used for inhibiting platelet  
XX CC aggregation, especially for treating cerebrovascular disorders. It is  
XX CC also used for treating cardiovascular disorders, especially acute  
XX CC myocardial infarction or angina. The protein is also used for inhibiting  
XX CC platelet aggregation before, during or after angioplasty, thrombolytic  
XX CC treatment or coronary bypass surgery, for maintaining blood vessel  
XX CC patency before, during or after coronary bypass surgery. It can also be  
XX CC used for inhibiting thrombosis, optionally associated with an  
XX CC inflammatory response, for inhibiting platelet adhesion to damaged  
XX CC vascular surfaces, for preventing platelet adhesion to prosthetic  
XX CC materials or devices, for inhibiting re-occlusion after angioplasty or  
XX CC thrombolysis, or for thrombolytic treatment of thrombi-containing  
XX CC platelet-rich aggregates.



SQ Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:  
Pred. No.: 9.47e+04 Length: 40  
Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservatives: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 20 Gaps: 0

US-09-375-514-22 (1-205) x AAV08903 (1-40)

QY 53 ProGlyHisThrProHisPro 59  
ID AAZ56179  
Db 1 CCAGGACGAGCCACATCCA 21

RESULT 44  
AAZ56179  
ID AAZ56179 standard; DNA; 40 BP.

AC AAZ56179;

XX 27-MAR-2000 (first entry)

DE Probe for human von Willebrand Factor (vWF) GPIb binding domain.

XX Von Willebrand Factor; vWF; GPIb binding domain; arteriosclerosis;  
KW platelet adhesion inhibitor; stenosis; cerebrovascular injury; human;  
KW thrombosis; cardiovascular injury; probe; ss.

XX Homo sapiens.

XX US6008193-A.

XX 28-DEC-1999.

XX 05-JUN-1995; 95US-0463682.

XX 30-NOV-1994; 94US-0347594.

PR 03-SEP-1991; 91US-0753815.

PR 22-JUN-1993; 93US-0080590.

PR 01-MAR-1990; 90US-0487767.

PR 01-MAR-1991; 91WO-US01416.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Richter T, Garfinkel L;

XX WPI; 2000-096379/08.

XX Preventing arteriosclerosis and stenosis using polypeptides derived  
XX from the human von Willebrand factor GPIb binding domain -

XX Example 1; Column 13; 65pp; English.

XX This is a probe for the human von Willebrand factor (vWF). The invention  
XX relates to methods of treating arteriosclerosis and stenosis using  
XX polypeptides derived from the human vWF GPIb binding domain. vWF is a  
XX large plasma protein which is synthesised in the endothelial cells of  
XX the blood vessels, and also by megakaryocytes which are the precursors  
XX of platelets. The treatment methods involve the administration of a  
XX polypeptide (see AAY67242 or AAY67243). These polypeptides contain a  
XX fragment of the vWF GPIb binding domain amino acid sequence. The  
XX polypeptides inhibit platelet adhesion and aggregation, therefore the  
XX methods may be used for preventing arteriosclerosis and stenosis (as a  
XX result of smooth muscle proliferation following vascular injury). The  
XX polypeptides may also be used for treating other cerebrovascular and  
XX cardiovascular injuries and thrombosis.

SQ Sequence 40 BP; 11 A; 14 C; 8 G; 7 T; 0 other;

Alignment Scores:  
Pred. No.: 9.47e+04 Length: 40

Score: 40.00 Matches: 6  
Percent Similarity: 85.71% Conservatives: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 3.62% Indels: 0  
DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAZ56179 (1-40)

QY 53 ProGlyHisThrProHisPro 59  
ID AAD17995  
Db 1 CCAGGACGAGCCACATCCA 21

RESULT 45  
AAD17995  
ID AAD17995 standard; DNA; 40 BP.

XX AAD17995;

XX 10-DEC-2001 (first entry)

DE A. fumigatus codon optimised phytase gene constructing phy52r PCR primer.

XX Phytase; Pichia cell; heterologous nucleotide; codon optimisation;  
KW PCR primer; ss.

XX Aspergillus fumigatus.

XX Synthetic.

XX WO200166693-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-DK00154.

PR 10-MAR-2000; 2000DK-0000392.

PR 15-MAR-2000; 2000DK-0000419.

XX (NOVO) NOVOZYMES AS.

XX Takagi S, Terui Y, Tsutsumi N, Taira R;

XX WPI; 2001-582273/65.

XX Novel Pichia cell useful for producing polypeptide of interest,  
XX comprises a copy of heterologous nucleotide sequence encoding  
XX polypeptide of interest -

XX Example 2; Page 53; 61pp; English.

XX The invention relates to a Pichia cell comprising at least one copy of  
XX heterologous nucleotide sequence encoding a polypeptide of interest,  
XX where the codon usage of the sequence has been adjusted to match the  
XX preferred codon usage of P. methanolica. The invention also relates to  
XX a method for producing high yields of heterologous codon optimised  
XX polypeptide in a Pichia cell. The Pichia cell is useful for producing  
XX a polypeptide of interest, where the polypeptide is encoded by a  
XX nucleotide sequence heterologous to P. methanolica. The present sequence  
XX is a PCR primer used for constructing Aspergillus fumigatus codon  
XX optimised phytase gene which is the heterologous DNA used in the  
XX invention.

SQ Sequence 40 BP; 9 A; 5 C; 17 G; 9 T; 0 other;

Alignment Scores:  
Pred. No.: 9.47e+04 Length: 40  
Score: 40.00 Matches: 7  
Percent Similarity: 66.67% Conservatives: 1  
Best Local Similarity: 58.33% Mismatches: 4  
Query Match: 3.62% Indels: 0  
DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x AAD17995 (1-40)

Qy 186 HlsHrTrpIlleGlnAspAsnGlyGlyTrpValGly 197  
 ||| :||| |||||  
 Db 2 CATGCTAGCGTTCAATGGAGGCTGCTGGTGGG 37

## RESULT 46

AAAL46236/C  
 ID AAL46236 standard; DNA; 40 BP.  
 XX  
 AC AAL46236;  
 XX  
 DT 15-AUG-2002 (first entry)  
 XX  
 DE Murine growth hormone coding sequence PCR primer SEQ ID NO: 16.  
 XX  
 KW Mouse; human; animal model; growth deficiency; cognitive function;  
 KW growth hormone; IGF-1; osteoporosis; cardiovascular disorder; dwarfism;  
 KW Illig-type deficiency; Kowarsky syndrome; diabetes; acromegaly;  
 KW gigantism; glomerulosclerosis; PCR; primer; ss.  
 XX  
 OS Mus musculus.  
 XX  
 WO200172119-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 02-APR-2001; 2001WO-EP03733.  
 XX  
 PR 31-MAR-2000; 2000DE-1016083.  
 XX  
 PA (INGE-) INGENIUM PHARM AG.  
 XX  
 PI Cornali E, Nehls MC, Schlueter V, Wattler F, Wattler S, Wolf S;  
 XX  
 DR WPI; 2001-616425/71.  
 XX  
 PT New animal model expressing a modified growth hormone has reduced body  
 PT weight and size and is useful to determine treatment for growth  
 PT hormone, particularly IGF-1 related conditions and diseases -  
 XX  
 PS Example 6; Page 74; 93pp; English.

XX The present invention relates to a mouse model expressing a modified  
 CC growth hormone and designated SMAL. The model is used to study diseases,  
 CC test prospective treatments and identify early detection markers  
 CC associated with abnormal growth hormone (GH) or IGF-1 activity,  
 CC particularly dwarfism, Laron syndrome, Illig-type deficiency, Kowarsky  
 CC syndrome, pituitary gland deficiency, reduced bone mineral density,  
 CC increased or insufficient body fat accumulation, diabetes, osteoporosis,  
 CC glomerulosclerosis, gigantism, acromegaly, information processing and  
 CC cognitive function defects, age-related memory and behaviour deficits,  
 CC glucose metabolism disorders and cardiovascular disorders. The present  
 CC sequence is a PCR primer described in the exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 40 BP; 5 A; 15 C; 16 G; 4 T; 0 other;

Alignment Scores:  
 Pred. No.: 9.47e+04 Length: 40  
 Score: 40.00 Matches: 7  
 Percent Similarity: 77.78% Conservative: 0  
 Best Local Similarity: 77.78% Mismatches: 2  
 Query Match: 3.62% Indels: 0  
 DB: 23 Gaps: 0

US-09-375-514-22 (1-205) x AAL46236 (1-40)

Qy 33 GlyAspValGlyAlaAlaProProGly 41  
 ||||| ||||| ||||| ||||| |||||

Db 40 GGAGACTCGGGAGCTGTGCTCCCGGC 14

## RESULT 47

AAA26253/C  
 ID AAA26253 standard; DNA; 23 BP.

XX AAA26253;  
 AC  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Bcl-2 antisense oligonucleotide sequence SEQ ID NO:2751.  
 XX  
 KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 WO9954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US08547.  
 XX  
 PR 20-APR-1998; 98US-0082404.  
 XX  
 PR 23-JUN-1998; 98US-0103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target  
 PT sequences, used to treat cancer -  
 XX  
 PS Example 9; Page 106; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(dithioate  
 CC link, having endonuclease activity. (A), and more generally any  
 CC catalytic nucleic acid (A') that modulates expression of the oestrogen  
 CC receptor gene, are used to treat cancer (particularly of breast or  
 CC endometrium), in vivo or by transforming cells ex vivo and implanting  
 CC treated cells, or for other conditions associated with levels of  
 CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)  
 CC can also be used to correlate inhibition of gene expression with  
 CC alterations in phenotype, particularly for identification of therapeutic  
 CC targets, and as research reagents (for RNA, in the same way that  
 CC restriction endonucleases are used with DNA). The combination of  
 CC modifications in (A) improves resistance to nucleases, binding affinity  
 CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor  
 CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their  
 CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen  
 CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent  
 CC their corresponding target sequences, and AAA26219 to AAA26271 represent  
 CC other ribozyme sequences and antisense oligonucleotides used in the  
 CC exemplification of the present invention.  
 XX

SQ Sequence 23 BP; 9 A; 9 C; 4 G; 1 T; 0 other;

Alignment Scores:  
 Pred. No.: 6.27e+04 Length: 23  
 Score: 39.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.53% Indels: 0  
 DB: 21 Gaps: 0

US-09-375-514-22 (1-205) x AAA26253 (1-23)

Qy 149 AlaPhePheGluPheGlyGly 155  
 ||||| ||||| ||||| |||||

Db 21 GCCTCTCTTCGAGTTCGGTGGG 1

RESULT 48  
 AAA26255/c  
 ID AAA26255 standard; DNA; 23 BP.  
 XX AC AAA26255;  
 XX 19-JUL-2000 (first entry)  
 XX DE Bcl-2 antisense oligonucleotide sequence SEQ ID NO:2753.  
 XX DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 XX anticancer; breast cancer; endometrium cancer; ss.  
 XX OS Homo sapiens.  
 XX PN WO9954459-A2.  
 XX PD 28-OCT-1999.  
 XX PF 19-APR-1999; 99WO-US08547.  
 XX PR 20-APR-1998; 98US-0082404.  
 XX PR 23-JUN-1998; 98US-0103636.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpelsky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;  
 XX DR WPI; 2000-013248/01.  
 XX PT New nucleic acids that interact, and optionally cleave, target  
 XX sequences, used to treat cancer -  
 XX PS Example 9; Page 106; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent their receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 23 BP; 9 A; 9 C; 4 G; 1 T; 0 other;

Alignment Scores:  
 Pred. No.: 23  
 Score: 6.27e+04  
 Length: 39.00  
 Matches: 7  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 3.53%  
 Indels: 0  
 Gaps: 0

US-09-375-514-22 (1-205) x AAA26255 (1-23)

QY 149 AlapheGluPheGly 155

Db 21 GCCTTCTTTGAGTTCGGTGGG 1  
 RESULT 49  
 AAA45301/c  
 ID AAA45301 standard; DNA; 27 BP.  
 XX AC AAA45301;  
 XX 10-SEP-2001 (first entry)  
 XX DE Human Bcl-2 mutagenic primer oligo-4 for S70D substitution.  
 XX KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200142459-A1.  
 XX PD 14-JUN-2001.  
 XX PF 07-DEC-2000; 2000WO-JP08667.  
 XX PR 09-DEC-1999; 99JP-0350427.  
 XX PA (HISM ) HISAMITSU PHARM CO LTD.  
 XX PI Shibazaki F, Kuma H;  
 XX DR WPI; 2001-381681/40.  
 XX PT New apoptosis inhibitors, useful for treating apoptosis related  
 XX disorders -  
 XX PS Example 1; Page 10; 43pp; Japanese.  
 XX CC The invention relates to an apoptosis inhibitor comprising the  
 CC amino acid sequence of Bcl-2 protein in which at least one serine  
 CC residue is substituted by alanine or aspartic acid. The protein has  
 CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence was used to  
 CC create a mutant Bcl-2 protein of the invention.  
 XX SQ Sequence 27 BP; 2 A; 8 C; 12 G; 5 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 27  
 Score: 7.38e+04  
 Length: 39.00  
 Matches: 8  
 Percent Similarity: 88.89%  
 Best Local Similarity: 88.89%  
 Query Match: 3.53%  
 DB: 22  
 Indels: 0  
 Gaps: 0  
 US-09-375-514-22 (1-205) x AAA45301 (1-27)  
 QY 66 ValAlaArgThrSerProLeuGlnThr 74  
 Db 27 GTCGCCAGGACCGCCGTCGAGACC 1  
 RESULT 50  
 AAA45303/c  
 ID AAA45303 standard; DNA; 27 BP.  
 XX AC AAA45303;  
 XX 10-SEP-2001 (first entry)  
 XX DE Human Bcl-2 mutagenic primer oligo-6 for S116D substitution.  
 XX KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant; primer; ss.

us-09-375-514-22.rng

Sun Jun 1 14:56:00 2003

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200142459-A1.  
 PN 14-JUN-2001.  
 PD 07-DEC-2000; 2000WO-JP08667.  
 XX 09-DEC-1999; 99JP-0350427.  
 PF (HISM) HISAMITSU PHARM CO LTD.  
 PR Shibazaki F, Kuma H;  
 XX WPI; 2001-381681/40.  
 DR New apoptosis inhibitors, useful for treating apoptosis related  
 PT disorders -  
 PS Example 1; Page 11; 43pp; Japanese.  
 XX The invention relates to an apoptosis inhibitor comprising the  
 CC amino acid sequence of Bcl-2 protein in which at least one serine  
 CC residue is substituted by alanine or aspartic acid. The protein has  
 CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence was used to  
 CC create a mutant Bcl-2 protein of the invention.  
 XX Sequence 27 BP; 5 A; 8 C; 9 G; 5 T; 0 other;

Alignment Scores:  
 Pred. No.: 7.38e+04 Length: 27  
 Score: 39.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 3.53% Indels: 0  
 DB: 22 Gaps: 0

US-09-375-514-22 (1-205) x ANH45303 (1-27)

Oy 112 PheAlaGluMetSerSerGlnLeuHis 120  
 Db 27 TTCGCCGAGATGGTCAGCCAGCTGCAC 1

Search completed: May 31, 2003, 22:29:38  
 Job time : 222 secs



66	24.8	0.5	28	6	I31539	I31539 Sequence 45	139	20.4	0.4	37	6	AR088795	AR088795 Sequence
67	24.8	0.5	28	13	AX031320	AX031320 Sequence	140	20.4	0.4	37	6	AR08875	AR08875 Sequence
68	24.4	0.5	26	6	AX477733	AX477733 Sequence	141	20.4	0.4	37	6	AX233376	AX233376 Sequence
69	24.4	0.5	26	6	AX477734	AX477734 Sequence	142	20.4	0.4	37	6	E05865	E05865 DNA sequence
70	24.2	0.5	30	6	E32218	E32218 Method for	c 143	20.4	0.4	39	6	AR0490	AR0490 oligonucleo
71	24	0.5	24	6	A22444	A22444 MBR primer.	c 144	20.4	0.4	39	6	A12569	A12569 fragment of
72	24	0.5	24	6	AX113808	AX113808 Sequence	c 145	20.2	0.4	33	6	I84406	I84406 Sequence 7
73	24	0.5	24	6	AX207607	AX207607 Sequence	146	20.4	0.4	33	6	A60097	A60097 Sequence 3
74	24	0.5	24	6	AX427160	AX427160 Sequence	147	20.4	0.4	20	6	A60104	A60104 Sequence 10
75	24	0.5	24	6	AX427162	AX427162 Sequence	148	20.4	0.4	20	6	A82351	A82351 Sequence 1
76	24	0.5	36	6	AR052608	AR052608 Sequence	149	20.4	0.4	20	6	A82352	A82352 Sequence 2
77	24	0.5	36	6	I96087	I96087 Sequence 6	c 150	20.4	0.4	20	6	A82353	A82353 Sequence 3
78	23.8	0.5	27	6	AR051255	AR051255 Sequence	c 151	20.4	0.4	20	6	A82354	A82354 Sequence 4
79	23.8	0.5	27	6	AX127802	AX127802 Sequence	152	20.4	0.4	20	6	AR021161	AR021161 Sequence
80	23.8	0.5	27	6	AX175237	AX175237 Sequence	c 153	20.4	0.4	20	6	AR021162	AR021162 Sequence
81	23.8	0.5	27	6	AX175241	AX175241 Sequence	c 154	20.4	0.4	20	6	AR052603	AR052603 Sequence
82	23.8	0.5	27	6	AX175302	AX175302 Sequence	c 155	20.4	0.4	20	6	AR052609	AR052609 Sequence
83	23.8	0.5	27	6	AX189457	AX189457 Sequence	c 156	20.4	0.4	20	6	AR052626	AR052626 Sequence
84	23.8	0.5	27	6	I28384	I28384 Sequence 23	c 157	20.4	0.4	20	6	AR052628	AR052628 Sequence
85	23.8	0.5	27	6	I31231	I31231 Sequence 14	158	20.4	0.4	20	6	AR170718	AR170718 Sequence
86	23.8	0.5	36	6	AR051239	AR051239 Sequence	159	20.4	0.4	20	6	AR170719	AR170719 Sequence
87	23.8	0.5	36	6	I28368	I28368 Sequence 7	c 160	20.4	0.4	20	6	AR170720	AR170720 Sequence
88	23.6	0.5	40	10	MW1MV26	X89143 M.musculus	c 161	20.4	0.4	20	6	AR170721	AR170721 Sequence
89	23	0.5	23	6	AR007290	AR007290 Sequence	c 162	20.4	0.4	20	6	AR176022	AR176022 Sequence
90	22.4	0.4	24	6	AR053546	AR053546 Sequence	c 163	20.4	0.4	20	6	AR176023	AR176023 Sequence
91	22.4	0.4	24	6	AR065873	AR065873 Sequence	164	20.4	0.4	20	6	AX045382	AX045382 Sequence
92	22.4	0.4	24	6	AR080355	AR080355 Sequence	c 165	20.4	0.4	20	6	AX045383	AX045383 Sequence
93	22.4	0.4	24	6	AR148310	AR148310 Sequence	c 166	20.4	0.4	20	6	AX045387	AX045387 Sequence
94	22.4	0.4	24	6	AX113809	AX113809 Sequence	c 167	20.4	0.4	20	6	AX207608	AX207608 Sequence
95	22	0.4	22	6	A76123	A76123 Sequence 3	168	20.4	0.4	20	6	AX211669	AX211669 Sequence
96	22	0.4	22	6	A76124	A76124 Sequence 4	c 169	20.4	0.4	20	6	AX211670	AX211670 Sequence
97	22	0.4	22	6	AR007292	AR007292 Sequence	170	20.4	0.4	20	6	AX224971	AX224971 Sequence
98	22	0.4	22	6	I16830	I16830 Sequence 1	171	20.4	0.4	20	6	AX224972	AX224972 Sequence
99	22	0.4	22	6	I16831	I16831 Sequence 2	172	20.4	0.4	20	6	AX224973	AX224973 Sequence
100	22	0.4	28	6	I50784	I50784 Sequence 15	173	20.4	0.4	20	6	AX224974	AX224974 Sequence
101	22	0.4	33	6	I31400	I31400 Sequence 31	174	20.4	0.4	20	6	AX224975	AX224975 Sequence
102	22	0.4	34	6	A45639	A45639 Sequence 33	175	20.4	0.4	20	6	AX224976	AX224976 Sequence
103	22	0.4	34	6	AR033092	AR033092 Sequence	176	20.4	0.4	20	6	AX224977	AX224977 Sequence
104	21.8	0.4	25	6	AX115976	AX115976 Sequence	177	20.4	0.4	20	6	AX224978	AX224978 Sequence
105	21.8	0.4	25	6	I31234	I31234 Sequence 14	178	20.4	0.4	20	6	AX224979	AX224979 Sequence
106	21.8	0.4	28	6	I50783	I50783 Sequence 14	179	20.4	0.4	20	6	AX224980	AX224980 Sequence
107	21.8	0.4	33	6	AX022524	AX022524 Sequence	180	20.4	0.4	20	6	AX224981	AX224981 Sequence
108	21.8	0.4	33	6	AX030812	AX030812 Sequence	181	20.4	0.4	20	6	AX224982	AX224982 Sequence
109	21.8	0.4	37	6	AR072973	AR072973 Sequence	182	20.4	0.4	20	6	AX224983	AX224983 Sequence
110	21.8	0.4	37	6	AR072975	AR072975 Sequence	183	20.4	0.4	20	6	AX224984	AX224984 Sequence
111	21.2	0.4	28	6	AR005121	AR005121 Sequence	184	20.4	0.4	20	6	AX224985	AX224985 Sequence
112	21.2	0.4	28	6	AR058248	AR058248 Sequence	185	20.4	0.4	20	6	AX224986	AX224986 Sequence
113	21.2	0.4	28	6	I42607	I42607 Sequence 10	186	20.4	0.4	20	6	AX224987	AX224987 Sequence
114	21	0.4	31	6	AX022526	AX022526 Sequence	187	20.4	0.4	20	6	AX224990	AX224990 Sequence
115	21	0.4	31	6	AX030814	AX030814 Sequence	c 188	20.4	0.4	20	6	AX277461	AX277461 Sequence
116	21	0.4	35	6	AR051292	AR051292 Sequence	c 189	20.4	0.4	20	6	I96082	I96082 Sequence 1
117	21	0.4	35	6	AR051293	AR051293 Sequence	c 190	20.4	0.4	20	6	I96088	I96088 Sequence 7
118	21	0.4	35	6	I16940	I16940 Sequence 9	c 191	20.4	0.4	24	6	AR020782	AR020782 Sequence
119	21	0.4	35	6	I16941	I16941 Sequence 10	c 192	20.4	0.4	28	6	I50781	I50781 Sequence 12
120	21	0.4	35	6	I45734	I45734 Sequence 9	c 193	20.4	0.4	31	6	AX249447	AX249447 Sequence
121	21	0.4	35	6	I45735	I45735 Sequence 10	c 194	20.4	0.4	38	6	E50766	E50766 Vector expr
122	20.8	0.4	24	6	AR070724	AR070724 Sequence	195	19.8	0.4	23	6	AR127801	AR127801 Sequence
123	20.8	0.4	24	6	AX104876	AX104876 Sequence	196	19.8	0.4	23	6	I31542	I31542 Sequence 45
124	20.8	0.4	24	6	AX175257	AX175257 Sequence	197	19.8	0.4	23	6	AX117832	AX117832 Sequence
125	20.8	0.4	24	6	AX175258	AX175258 Sequence	c 198	19.8	0.4	28	6	AR120088	AR120088 Sequence
126	20.8	0.4	24	6	I17110	I17110 Sequence 3	c 199	19.8	0.4	28	6	AR120089	AR120089 Sequence
127	20.8	0.4	24	6	I31533	I31533 Sequence 44	200	19.8	0.4	39	6	A08918	A08918 H.sapiens (
128	20.8	0.4	24	6	I62399	I62399 Sequence 3	c 201	19.8	0.4	40	6	AX027921	AX027921 Sequence
129	20.8	0.4	25	6	AX117836	AX117836 Sequence	c 202	19.8	0.4	40	6	AX028180	AX028180 Sequence
130	20.8	0.4	40	6	AR074704	AR074704 Sequence	203	19.6	0.4	30	6	I84401	I84401 Sequence 2
131	20.8	0.4	40	6	AR074705	AR074705 Sequence	204	19.6	0.4	31	6	A01419	A01419 Malaria par
132	20.8	0.4	40	6	AR184470	AR184470 Sequence	205	19.6	0.4	39	6	AR184233	AR184233 Sequence
133	20.8	0.4	40	6	AX406837	AX406837 Sequence	206	19.6	0.4	39	6	AR184354	AR184354 Sequence
134	20.6	0.4	27	6	AR004426	AR004426 Sequence	207	19.6	0.4	39	6	AX127942	AX127942 Sequence
135	20.6	0.4	27	6	I43661	I43661 Sequence 13	208	19.6	0.4	40	6	E04403	E04403 Probes for
136	20.6	0.4	27	6	I86720	I86720 Sequence 8	c 209	19.4	0.4	21	6	AR070725	AR070725 Sequence
137	20.6	0.4	28	6	AR072974	AR072974 Sequence	c 210	19.4	0.4	21	6	I17111	I17111 Sequence 4
138	20.4	0.4	37	6	AR058971	AR058971 Sequence	c 211	19.4	0.4	21	6	I62400	I62400 Sequence 4

212	19.4	0.4	27	6	A63581	A63581 Sequence 22	285	19	0.4	40	6	AX235336	AX235336 Sequence
213	19.4	0.4	30	6	A43129	A43129 Sequence 15	c 286	19	0.4	40	6	AX299737	AX299737 Sequence
214	19.4	0.4	30	6	AX351711	AX351711 Sequence	287	18.8	0.4	22	6	AX031293	AX031293 Sequence
215	19.4	0.4	32	6	AR051291	AR051291 Sequence	288	18.8	0.4	22	6	I31213	I31213 Sequence
216	19.4	0.4	32	6	E32225	E32225 Method for	c 289	18.8	0.4	22	13	AX031319	AX031319 Sequence
217	19.4	0.4	32	6	I16939	I16939 Sequence 8	c 290	18.8	0.4	23	6	AX116678	AX116678 Sequence
218	19.4	0.4	32	6	I45733	I45733 Sequence 8	c 291	18.8	0.4	24	6	AR010035	AR010035 Sequence
219	19.4	0.4	33	6	A31589	A31589 Synthetic m	c 292	18.8	0.4	24	6	AR034770	AR034770 Sequence
220	19.4	0.4	35	6	AR051295	AR051295 Sequence	c 293	18.8	0.4	24	6	AX116747	AX116747 Sequence
221	19.4	0.4	35	6	AR051298	AR051298 Sequence	c 294	18.8	0.4	24	6	I24746	I24746 Sequence 9
222	19.4	0.4	35	6	I16943	I16943 Sequence 12	c 295	18.8	0.4	25	6	AR028113	AR028113 Sequence
223	19.4	0.4	35	6	I16946	I16946 Sequence 15	c 296	18.8	0.4	25	6	AR030289	AR030289 Sequence
224	19.4	0.4	35	6	I45737	I45737 Sequence 12	c 297	18.8	0.4	25	6	AX117828	AX117828 Sequence
225	19.4	0.4	35	6	I45740	I45740 Sequence 15	c 298	18.8	0.4	25	6	I42108	I42108 Sequence 3
226	19.4	0.4	36	6	AX402097	AX402097 Sequence	c 299	18.8	0.4	31	6	AX220938	AX220938 Sequence
227	19.4	0.4	36	6	AX403811	AX403811 Sequence	c 300	18.8	0.4	33	6	AX068144	AX068144 Sequence
228	19.4	0.4	37	6	AX180731	AX180731 Sequence	301	18.8	0.4	35	6	AR071305	AR071305 Sequence
229	19.4	0.4	38	6	A05163	A05163 Nucleotide	302	18.8	0.4	35	6	AR126789	AR126789 Sequence
230	19.4	0.4	38	6	AR154325	AR154325 Sequence	303	18.8	0.4	35	6	AR202446	AR202446 Sequence
231	19.4	0.4	39	6	AR022264	AR022264 Sequence	304	18.8	0.4	36	6	AX183980	AX183980 Sequence
232	19.4	0.4	39	6	AR031440	AR031440 Sequence	c 305	18.8	0.4	38	6	AR045842	AR045842 Sequence
233	19.4	0.4	39	6	AR073013	AR073013 Sequence	c 306	18.8	0.4	38	6	I52894	I52894 Sequence 63
234	19.4	0.4	39	6	AR078278	AR078278 Sequence	c 307	18.8	0.4	39	6	A08489	A08489 B.taurus ge
235	19.4	0.4	39	6	AR154654	AR154654 Sequence	c 308	18.8	0.4	39	6	A08491	A08491 oligonucleo
236	19.4	0.4	39	6	I16079	I16079 Sequence 40	c 309	18.8	0.4	39	6	AI2570	AI2570 fragment of
237	19.4	0.4	39	6	I84408	I84408 Sequence 9	310	18.8	0.4	40	6	AR050485	AR050485 Sequence
238	19.2	0.4	24	6	AR010030	AR010030 Sequence	311	18.8	0.4	40	6	AR124613	AR124613 Sequence
239	19.2	0.4	24	6	AR034765	AR034765 Sequence	c 312	18.8	0.4	40	6	AX137541	AX137541 Sequence
240	19.2	0.4	24	6	I24743	I24743 Sequence 6	313	18.8	0.4	40	6	E28168	E28168 Protein bin
241	19.2	0.4	27	6	AX207515	AX207515 Sequence	c 314	18.6	0.4	28	6	AR117902	AR117902 Sequence
242	19.2	0.4	27	6	AX207519	AX207519 Sequence	315	18.6	0.4	28	6	AR156898	AR156898 Sequence
243	19.2	0.4	27	6	AX207523	AX207523 Sequence	316	18.6	0.4	28	6	AX128360	AX128360 Sequence
244	19.2	0.4	27	6	AX207553	AX207553 Sequence	c 317	18.6	0.4	30	6	AR016486	AR016486 Sequence
245	19.2	0.4	27	6	AX207557	AX207557 Sequence	318	18.6	0.4	30	6	AR028226	AR028226 Sequence
246	19.2	0.4	28	6	AR120087	AR120087 Sequence	c 319	18.6	0.4	30	6	AR078334	AR078334 Sequence
247	19.2	0.4	34	6	A63578	A63578 Sequence 19	320	18.6	0.4	30	6	AR138629	AR138629 Sequence
248	19.2	0.4	35	6	A63566	A63566 Sequence 7	c 321	18.6	0.4	30	6	AR173054	AR173054 Sequence
249	19.2	0.4	35	6	AR051296	AR051296 Sequence	c 322	18.6	0.4	30	6	AX267025	AX267025 Sequence
250	19.2	0.4	35	6	AR051302	AR051302 Sequence	c 323	18.6	0.4	31	6	AX248532	AX248532 Sequence
251	19.2	0.4	35	6	I16944	I16944 Sequence 13	c 324	18.6	0.4	33	6	AX107320	AX107320 Sequence
252	19.2	0.4	35	6	I16950	I16950 Sequence 19	325	18.6	0.4	33	6	E09084	E09084 DNA encodin
253	19.2	0.4	35	6	I45738	I45738 Sequence 13	326	18.6	0.4	34	6	I39756	I39756 Sequence 29
254	19.2	0.4	36	6	I45744	I45744 Sequence 19	c 327	18.6	0.4	35	6	AR051303	AR051303 Sequence
255	19.2	0.4	36	6	I68112	I68112 Sequence 4	c 328	18.6	0.4	35	6	I16951	I16951 Sequence 20
256	19.2	0.4	37	6	AX183681	AX183681 Sequence	c 329	18.6	0.4	35	6	I45745	I45745 Sequence 20
257	19.2	0.4	4	6	I86255	I86255 Sequence 9	c 330	18.6	0.4	36	6	E03618	E03618 DNA primer
258	19	0.4	19	6	AR007287	AR007287 Sequence	c 331	18.6	0.4	36	9	S63150	S63150 hprt-hypoxa
259	19	0.4	19	6	AR007297	AR007297 Sequence	332	18.6	0.4	39	6	AX068141	AX068141 Sequence
260	19	0.4	19	6	AR007298	AR007298 Sequence	c 333	18.6	0.4	40	6	AR027330	AR027330 Sequence
261	19	0.4	19	6	AR007300	AR007300 Sequence	334	18.6	0.4	40	6	AR203020	AR203020 Sequence
262	19	0.4	19	6	AX083694	AX083694 Sequence	335	18.6	0.4	40	6	AX099682	AX099682 Sequence
263	19	0.4	20	6	AX224989	AX224989 Sequence	336	18.6	0.4	40	6	I82317	I82317 Sequence 2
264	19	0.4	32	6	AR091462	AR091462 Sequence	c 337	18.6	0.4	40	6	AX045385	AX045385 Sequence
265	19	0.4	32	6	AR104413	AR104413 Sequence	338	18.4	0.4	20	6	AX224988	AX224988 Sequence
266	19	0.4	33	6	AX046492	AX046492 Sequence	c 339	18.4	0.4	21	12	AB068223	AB068223 Synthetic
267	19	0.4	35	6	AX104579	AX104579 Sequence	340	18.4	0.4	25	6	AX043334	AX043334 Sequence
268	19	0.4	35	6	AX355144	AX355144 Sequence	c 341	18.4	0.4	29	6	AX430216	AX430216 Sequence
269	19	0.4	36	6	I09401	I09401 Sequence 2	342	18.4	0.4	31	6	AR016489	AR016489 Sequence
270	19	0.4	38	6	AR125937	AR125937 Sequence	343	18.4	0.4	31	6	AR101054	AR101054 Sequence
271	19	0.4	38	6	AX009599	AX009599 Sequence	c 344	18.4	0.4	32	6	I08576	I08576 Sequence 21
272	19	0.4	38	6	I24304	I24304 Sequence 91	c 345	18.4	0.4	35	6	AR061524	AR061524 Sequence
273	19	0.4	38	6	I49650	I49650 Sequence 2	c 346	18.4	0.4	35	6	AR108423	AR108423 Sequence
274	19	0.4	38	6	I56644	I56644 Sequence 2	347	18.4	0.4	35	6	I16380	I16380 Sequence 20
275	19	0.4	39	6	AR140900	AR140900 Sequence	c 348	18.4	0.4	35	6	I66866	I66866 Sequence 20
276	19	0.4	39	6	AR150850	AR150850 Sequence	c 349	18.4	0.4	35	6	I84960	I84960 Sequence 20
277	19	0.4	39	6	AX137540	AX137540 Sequence	c 350	18.4	0.4	36	6	AR033954	AR033954 Sequence
278	19	0.4	39	6	I31419	I31419 Sequence 33	c 351	18.4	0.4	36	6	AR084542	AR084542 Sequence
279	19	0.4	39	6	I65730	I65730 Sequence 90	c 352	18.4	0.4	36	6	AR175087	AR175087 Sequence
280	19	0.4	39	6	I67962	I67962 Sequence 90	c 353	18.4	0.4	36	6	AX032535	AX032535 Sequence
281	19	0.4	39	6	I90181	I90181 Sequence 88	354	18.4	0.4	36	6	I13627	I13627 Sequence 12
282	19	0.4	39	9	HSCDB5706	HSCDB5706	355	18.4	0.4	36	6	I63478	I63478 Sequence 9
283	19	0.4	39	10	MUSFCBYBL	M61139 M.musculus	356	18.4	0.4	37	6	AX106972	AX106972 Sequence
284	19	0.4	40	6	AR089808	AR089808 Sequence	c 357	18.4	0.4	37	6	I29931	I29931 Sequence 44

c 358	18.4	0.4	39	6	Al2568	Al12568 fragment of	c 431	18	0.4	18	6	AX020954	Sequence
c 359	18.4	0.4	39	6	AX135021	AX135021 Sequence	c 432	18	0.4	18	6	AX040169	Sequence
c 360	18.4	0.4	39	6	AX183775	AX183775 Sequence	c 433	18	0.4	18	6	AX040403	Sequence
c 361	18.4	0.4	39	6	E00478	E00478 DNA encodin	c 434	18	0.4	18	6	AX063576	Sequence
c 362	18.4	0.4	40	6	A31818	A31818 Synthetic P	c 435	18	0.4	18	6	AX081353	Sequence
c 363	18.4	0.4	40	6	A31822	A31822 Synthetic m	c 436	18	0.4	18	6	AX083693	Sequence
c 364	18.4	0.4	40	6	A48799	A48799 Sequence 6	c 437	18	0.4	18	6	AX088930	Sequence
c 365	18.4	0.4	40	6	AX027922	AX027922 Sequence	c 438	18	0.4	18	6	AX103809	Sequence
c 366	18.4	0.4	40	6	AX028181	AX028181 Sequence	c 439	18	0.4	18	6	AX103862	Sequence
c 367	18.4	0.4	24	6	AX117030	AX117030 Sequence	c 440	18	0.4	18	6	AX103863	Sequence
c 368	18.2	0.4	25	6	AX043448	AX043448 Sequence	c 441	18	0.4	18	6	AX103899	Sequence
c 369	18.2	0.4	27	6	AR103579	AR103579 Sequence	c 442	18	0.4	18	6	AX105211	Sequence
c 370	18.2	0.4	28	6	A05379	A05379 Synthetic o	c 443	18	0.4	18	6	AX135635	Sequence
c 371	18.2	0.4	28	6	A05380	A05380 Synthetic o	c 444	18	0.4	18	6	AX283183	Sequence
c 372	18.2	0.4	28	6	A09586	A09586 Oligonucleo	c 445	18	0.4	18	6	AX283250	Sequence
c 373	18.2	0.4	28	6	A09587	A09587 Oligonucleo	c 446	18	0.4	18	6	AX355727	Sequence
c 374	18.2	0.4	31	6	A07573	A07573 p11197 DNA	c 447	18	0.4	18	6	AX355728	Sequence
c 375	18.2	0.4	31	6	A07575	A07575 p11197 DNA	c 448	18	0.4	18	6	AX455638	Sequence
c 376	18.2	0.4	31	6	A08914	A08914 H.sapiens (	c 449	18	0.4	18	6	AX468484	Sequence
c 377	18.2	0.4	31	6	AR168783	AR168783 Sequence	c 450	18	0.4	18	6	BD008994	Inhibitio
c 378	18.2	0.4	31	6	AR200252	AR200252 Sequence	c 451	18	0.4	18	6	BD009103	Immunosti
c 379	18.2	0.4	31	6	I27777	I27777 Sequence 9	c 452	18	0.4	18	6	I96098	Sequence 17
c 380	18.2	0.4	32	6	AX184217	AX184217 Sequence	c 453	18	0.4	19	6	AX083695	Sequence
c 381	18.2	0.4	33	6	AR099615	AR099615 Sequence	c 454	18	0.4	19	6	AX453854	Sequence
c 382	18.2	0.4	33	6	AR120128	AR120128 Sequence	c 455	18	0.4	20	6	AR062659	Sequence
c 383	18.2	0.4	34	6	AR031717	AR031717 Sequence	c 456	18	0.4	20	6	AR104762	Sequence
c 384	18.2	0.4	36	6	AR033953	AR033953 Sequence	c 457	18	0.4	20	6	AR105584	Sequence
c 385	18.2	0.4	36	6	AR175086	AR175086 Sequence	c 458	18	0.4	20	6	AR123246	Sequence
c 386	18.2	0.4	36	6	AX032534	AX032534 Sequence	c 459	18	0.4	20	6	AR182888	Sequence
c 387	18.2	0.4	36	6	AX083708	AX083708 Sequence	c 460	18	0.4	20	6	AX103895	Sequence
c 388	18.2	0.4	37	6	AX052930	AX052930 Sequence	c 461	18	0.4	20	6	AX355729	Sequence
c 389	18.2	0.4	37	6	AX352060	AX352060 Sequence	c 462	18	0.4	20	6	I20661	Sequence 59
c 390	18.2	0.4	38	6	A73301	A73301 Sequence 17	c 463	18	0.4	20	6	I33354	Sequence 59
c 391	18.2	0.4	38	6	AR009851	AR009851 Sequence	c 464	18	0.4	23	6	AX083687	Sequence
c 392	18.2	0.4	38	6	AR061042	AR061042 Sequence	c 465	18	0.4	23	6	AX083688	Sequence
c 393	18.2	0.4	38	6	AR161675	AR161675 Sequence	c 466	18	0.4	25	6	AR070732	Sequence
c 394	18.2	0.4	38	6	AX079123	AX079123 Sequence	c 467	18	0.4	25	6	I17118	Sequence 13
c 395	18.2	0.4	38	6	AX079169	AX079169 Sequence	c 468	18	0.4	25	6	I50782	Sequence 13
c 396	18.2	0.4	39	6	AR107428	AR107428 Sequence	c 469	18	0.4	25	6	I62407	Sequence 13
c 397	18.2	0.4	39	6	AR120174	AR120174 Sequence	c 470	18	0.4	26	6	I72458	Sequence 42
c 398	18.2	0.4	39	6	AR126172	AR126172 Sequence	c 471	18	0.4	27	6	AX196894	Sequence
c 399	18.2	0.4	39	6	AR156710	AR156710 Sequence	c 472	18	0.4	28	6	A61962	Sequence 2
c 400	18.2	0.4	39	6	AR168476	AR168476 Sequence	c 473	18	0.4	30	6	AR016491	Sequence
c 401	18.2	0.4	39	6	AR177988	AR177988 Sequence	c 474	18	0.4	30	6	AR028195	Sequence
c 402	18.2	0.4	39	6	AR179206	AR179206 Sequence	c 475	18	0.4	30	6	AR078336	Sequence
c 403	18.2	0.4	39	6	AR209014	AR209014 Sequence	c 476	18	0.4	30	6	AR138598	Sequence
c 404	18.2	0.4	39	6	AX383780	AX383780 Sequence	c 477	18	0.4	30	6	AR173056	Sequence
c 405	18.2	0.4	39	6	BD007652	BD007652 Delta-end	c 478	18	0.4	30	6	I26957	Sequence 6
c 406	18.2	0.4	39	6	EL1415	EL1415 Primer. 9/1	c 479	18	0.4	31	6	AX236752	Sequence
c 407	18.2	0.4	39	9	HSTCARB6	Z35675 H.sapiens (	c 480	18	0.4	33	6	I07628	Sequence 4
c 408	18.2	0.4	40	6	AR030569	AR030569 Sequence	c 481	18	0.4	35	6	AX008888	Sequence
c 409	18.2	0.4	40	6	AR050322	AR050322 Sequence	c 482	18	0.4	35	6	AX419884	Sequence
c 410	18.2	0.4	40	6	AR204903	AR204903 Sequence	c 483	18	0.4	35	6	E05782	Primer. 9/1
c 411	18.2	0.4	40	6	AX279903	AX279903 Sequence	c 484	18	0.4	35	6	E05783	Primer. 9/1
c 412	18.2	0.4	40	6	AX456322	AX456322 Sequence	c 485	18	0.4	35	6	I35032	Sequence 11
c 413	18.2	0.4	40	6	AX472253	AX472253 Sequence	c 486	18	0.4	36	6	I34917	Sequence 3
c 414	18.2	0.4	40	8	YSCMP022	J01513 Yeast (S.ce	c 487	18	0.4	37	6	AX015583	Sequence
c 415	18	0.4	18	6	A56835	A56835 Sequence 14	c 488	18	0.4	38	6	AR168776	Sequence
c 416	18	0.4	18	6	A56835	A56835 Sequence 33	c 489	18	0.4	38	6	AR168778	Sequence
c 417	18	0.4	18	6	A56855	A56855 Sequence 34	c 490	18	0.4	38	6	AR200245	Sequence
c 418	18	0.4	18	6	AR052619	AR052619 Sequence	c 491	18	0.4	38	6	AR200247	Sequence
c 419	18	0.4	18	6	AR052624	AR052624 Sequence	c 492	18	0.4	38	6	BD007241	Sequence
c 420	18	0.4	18	6	AR096230	AR096230 Sequence	c 493	18	0.4	38	6	E14033	Probe. 7/19
c 421	18	0.4	18	6	AR096250	AR096250 Sequence	c 494	18	0.4	38	6	I27770	Sequence 2
c 422	18	0.4	18	6	AR096251	AR096251 Sequence	c 495	18	0.4	38	6	I27772	Sequence 4
c 423	18	0.4	18	6	AR116926	AR116926 Sequence	c 496	18	0.4	39	6	AX080628	Sequence
c 424	18	0.4	18	6	AR140496	AR140496 Sequence	c 497	18	0.4	39	6	I31761	Sequence 14
c 425	18	0.4	18	6	AR146347	AR146347 Sequence	c 498	18	0.4	40	6	A93812	Sequence 5
c 426	18	0.4	18	6	AR146392	AR146392 Sequence	c 499	18	0.4	40	6	A93813	Sequence 6
c 427	18	0.4	18	6	AR154716	AR154716 Sequence	c 500	18	0.4	40	6	AR053646	Sequence
c 428	18	0.4	18	6	AR167448	AR167448 Sequence							
c 429	18	0.4	18	6	AX015198	AX015198 Sequence							
c 430	18	0.4	18	6	AX020948	AX020948 Sequence							

ALIGNMENTS



RESULT 1  
AX377551  
LOCUS AX377551 39 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 28 from Patent WO0212553.  
ACCESSION AX377551  
VERSION AX377551.1 GI:19573737  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdoerf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 28 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1..39  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 7 a 21 c 9 g 2 t  
ORIGIN  
Query Match 0.8%; Score 39; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1613 AGCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 1651  
|||||  
Db 1 AGCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 39  
|||||  
RESULT 2  
AX377552  
LOCUS AX377552 39 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 29 from Patent WO0212553.  
ACCESSION AX377552  
VERSION AX377552.1 GI:19573738  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdoerf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 29 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1..39  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 7 a 20 c 9 g 3 t  
ORIGIN  
Query Match 0.7%; Score 37.4; DB 6; Length 39;  
Best Local Similarity 97.4%; Pred. No. 5.8e+03;  
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1613 AGCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 1651  
|||||  
Db 1 AGCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 39  
|||||  
RESULT 3  
AR007288  
LOCUS AR007288 37 bp DNA linear  
DEFINITION Sequence 2 from patent US 5750390.  
ACCESSION AR007288

AR007288.1 GI:3966772  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Thompson,J.D. and Draper,K.G.  
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL Patent: US 5750390-A 2 12-MAY-1998;  
FEATURES  
source 1..37  
Location/Qualifiers  
/organism="unknown"  
BASE COUNT 2 a 12 c 12 g 11 t  
ORIGIN  
Query Match 0.7%; Score 37; DB 6; Length 37;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1415 GCGGAGAGTGCGGTGGCCCCCGTGGCTTTTCTCT 1451  
|||||  
Db 1 GCGGAGAGTGCGGTGGCCCCCGTGGCTTTTCTCT 37  
|||||  
RESULT 4  
AX377550/c  
LOCUS AX377550 39 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 27 from Patent WO0212553.  
ACCESSION AX377550  
VERSION AX377550.1 GI:19573736  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE 1  
AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdoerf,H. and Muth,J.  
TITLE Method for detecting mutations in nucleotide sequences  
JOURNAL Patent: WO 0212553-A 27 14-FEB-2002;  
Nanogen Recognomics GmbH (DE)  
FEATURES  
source 1..39  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 4 a 8 c 21 g 6 t  
ORIGIN  
Query Match 0.7%; Score 37; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1615 CCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 1651  
|||||  
Db 39 CCCGGGCACACGCCGCCATCCAGCGCATCCCGGACC 3  
|||||  
RESULT 5  
AR007301  
LOCUS AR007301 36 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 15 from patent US 5750390.  
ACCESSION AR007301  
VERSION AR007301.1 GI:3966785  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Thompson,J.D. and Draper,K.G.  
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL Patent: US 5750390-A 15 12-MAY-1998;

FEATURES source Location/Qualifiers  
1. .36  
BASE COUNT 10 a 13 c 8 g 5 t  
ORIGIN

Query Match 0.7%; Score 36; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 ACCTGAACGGCAGCTGCACACCTGGATCCAGGATA 2032  
|||||  
Db 1 ACCTGAACGGCAGCTGCACACCTGGATCCAGGATA 36  
|||||

RESULT 6  
AR007306  
LOCUS  
DEFINITION Sequence 20 from patent US 5750390.  
ACCESSION AR007306  
VERSION AR007306.1 GI:3966790  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 35)  
AUTHORS Thompson, J.D. and Draper, K.G.  
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL Patent: US 5750390-A 20 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1. .35  
BASE COUNT 14 a 10 c 6 g 5 t  
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2180 GTCACATGCTGCTGCCCAACAAATATGCAAGG 2214  
|||||  
Db 1 GTCACATGCTGCTGCCCAACAAATATGCAAGG 35  
|||||

RESULT 7  
AR052604  
LOCUS  
DEFINITION Sequence 2 from patent US 5831066.  
ACCESSION AR052604  
VERSION AR052604.1 GI:5975968  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 35)  
AUTHORS Reed, J.C.  
TITLE Regulation of bcl-2 gene expression  
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1. .35  
BASE COUNT 6 a 8 c 13 g 8 t  
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTCTCTCTGGGAGGATGCGCACCGCTGGGAGA 1476  
|||||  
Db 1 CTTTCTCTCTGGGAGGATGCGCACCGCTGGGAGA 35  
|||||

RESULT 8  
I96083  
LOCUS  
DEFINITION Sequence 2 from patent US 5734033.  
ACCESSION I96083  
VERSION I96083.1 GI:3940553  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 35)  
AUTHORS Reed, J.  
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression  
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;  
FEATURES Location/Qualifiers  
source 1. .35  
BASE COUNT 6 a 8 c 13 g 8 t  
ORIGIN

Query Match 0.7%; Score 35; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTCTCTCTGGGAGGATGCGCACCGCTGGGAGA 1476  
|||||  
Db 1 CTTTCTCTCTGGGAGGATGCGCACCGCTGGGAGA 35  
|||||

RESULT 9  
AR007302  
LOCUS  
DEFINITION Sequence 16 from patent US 5750390.  
ACCESSION AR007302  
VERSION AR007302.1 GI:3966786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Thompson, J.D. and Draper, K.G.  
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL Patent: US 5750390-A 16 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1. /34  
BASE COUNT 6 a 9 c 11 g 8 t  
ORIGIN

Query Match 0.7%; Score 34; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2043 GGATGCTTTGTGGAACTGTACGGCCCCCAGCATG 2076  
|||||  
Db 1 GGATGCTTTGTGGAACTGTACGGCCCCCAGCATG 34  
|||||

RESULT 10  
AR007307  
LOCUS  
DEFINITION Sequence 21 from patent US 5750390.  
ACCESSION AR007307  
VERSION AR007307.1 GI:3966791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Thompson, J.D. and Draper, K.G.  
TITLE Method and reagent for treatment of diseases caused by expression

of the bcl-2 gene  
Patent: US 5750390-A 21 12-MAY-1998;  
Location/Qualifiers

FEATURES  
source  
1. .33  
/organism="unknown"

BASE COUNT  
ORIGIN  
14 a 5 c 6 g 9 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 2.6e+04; Length 34;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATATGCAATGTCAGTGTACCATGAACAAA 2268

Db 1 AATATGCAATGTCAGTGTACCATGAACAAA 34

RESULT 11

LOCUS A56864 33 bp DNA linear PAT 03-MAR-1998

DEFINITION Sequence 43 from Patent WO9627663.

ACCESSION A56864

VERSION A56864.1 GI:3712876

KEYWORDS

SOURCE

ORGANISM

unidentified.

unclassified.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .33

/organism="unidentified"

/db\_xref="taxon:32644"

BASE COUNT

ORIGIN

9 a 6 c 6 g 12 t

Query Match

Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4289 GCAATCCGCATTAAATTCAGTATTCAGGAT 4321

Db 1 GCAATCCGCATTAAATTCAGTATTCAGGAT 33

RESULT 12

LOCUS AR007291

DEFINITION Sequence 5 from patent US 5750390.

ACCESSION AR007291

VERSION AR007291.1 GI:3966775

KEYWORDS

SOURCE

ORGANISM

Unknown.

unclassified.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .33

/organism="unknown"

BASE COUNT

ORIGIN

5 a 16 c 7 g 5 t

Query Match

0.6%; Score 33; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1592 CACGGGCAATCTCTCTCCAGCCGCGCACAC 1624

Db 1 CACGGGCAATCTCTCTCCAGCCGCGCACAC 33

RESULT 13

LOCUS AR096260

DEFINITION Sequence 44 from patent US 6005095.

ACCESSION AR096260

VERSION AR096260.1 GI:10024906

KEYWORDS

SOURCE

ORGANISM

Unknown.

unclassified.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .33

/organism="unknown"

BASE COUNT

ORIGIN

9 a 6 c 6 g 12 t

Query Match

Best Local Similarity 100.0%; Pred. No. 4e+04; Length 33;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4289 GCAATCCGCATTAAATTCAGTATTCAGGAT 4321

Db 1 GCAATCCGCATTAAATTCAGTATTCAGGAT 33

RESULT 14

LOCUS AX207593

DEFINITION Sequence 2 from Patent WO0157205.

ACCESSION AX207593

VERSION AX207593.1 GI:15422299

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .33

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT

ORIGIN

15 a 4 c 40 g 7 t

Query Match

Best Local Similarity 94.4%; Pred. No. 4.5e+04; Length 36;

Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4098 CAAAGCATCTCTGAGAGGTGAGATAGCCCTGAGT 4133

Db 1 CAAAGCATCTCTGAGAGGTGAGATAGCCCTGAGT 36

RESULT 15  
A56840  
LOCUS  
DEFINITION  
Accession  
A56840  
VERSION  
A56840.1 GI:3712852  
KEYWORDS  
SOURCE  
ORGANISM  
unidentified.  
unidentified  
unclassified.  
REFERENCE  
1 (bases 1 to 30)  
AUTHORS  
Capaccioli, S., Morelli, S., and Nicolin, A.  
TITLE  
AN ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR CELLS HAVING A T(14;18) TRANSLLOCATION AND OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND TREATMENT OF SAID TUMOR CELLS  
JOURNAL  
Patent: WO 9627663-A 19 12-SEP-1996;  
COMMENT  
CONSISTO NAZIONALE RICERCA (IT)  
Other publication AU 4944296 960923.  
FEATURES  
Location/Qualifiers  
1..30  
Source  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT  
3 a 9 c 6 g 12 t  
ORIGIN  
Query Match  
Best Local Similarity 0.6%; Score 30; DB 6; Length 30;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4256 GACCTTGTTCCTGAAGTTTCCTCGTCCC 4285  
|||||  
Db 1 GACCTTGTTCCTGAAGTTTCCTCGTCCC 30  
RESULT 16  
AR096235  
LOCUS  
DEFINITION  
Accession  
AR096235  
VERSION  
AR096235.1 GI:10024856  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 30)  
AUTHORS  
Capaccioli, S., Morelli, S., and Nicolin, A.  
TITLE  
Antisense transcript associated to tumor cells having a T(14;18) translocation and oligodeoxynucleotides useful in the diagnosis and treatment of said tumor cells  
JOURNAL  
Patent: US 6005095-A 19 21-DEC-1999;  
FEATURES  
Location/Qualifiers  
1..30  
Source  
/organism="unknown"  
BASE COUNT  
3 a 9 c 6 g 12 t  
ORIGIN  
Query Match  
Best Local Similarity 0.6%; Score 30; DB 6; Length 30;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4256 GACCTTGTTCCTGAAGTTTCCTCGTCCC 4285  
|||||  
Db 1 GACCTTGTTCCTGAAGTTTCCTCGTCCC 30  
RESULT 17  
AR096239  
LOCUS  
DEFINITION  
Accession  
AR096239  
VERSION  
AR096239.1 GI:10024864  
KEYWORDS  
SOURCE  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 28)  
AUTHORS  
Thompson, J.D. and Draper, K.G.  
TITLE  
Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL  
Patent: US 5750390-A 8 12-MAY-1998;  
FEATURES  
Location/Qualifiers  
1..28  
Source  
/organism="unknown"  
BASE COUNT  
3 a 13 c 7 g 5 t  
ORIGIN

ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 30)  
AUTHORS  
Capaccioli, S., Morelli, S., and Nicolin, A.  
TITLE  
Antisense transcript associated to tumor cells having a T(14;18) translocation and oligodeoxynucleotides useful in the diagnosis and treatment of said tumor cells  
JOURNAL  
Patent: US 6005095-A 23 21-DEC-1999;  
FEATURES  
Location/Qualifiers  
1..30  
Source  
/organism="unknown"  
BASE COUNT  
3 a 9 c 6 g 12 t  
ORIGIN  
Query Match  
Best Local Similarity 0.6%; Score 30; DB 6; Length 30;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4256 GACCTTGTTCCTGAAGTTTCCTCGTCCC 4285  
|||||  
Db 1 GACCTTGTTCCTGAAGTTTCCTCGTCCC 30  
RESULT 18  
I31503  
LOCUS  
DEFINITION  
Accession  
I31503  
VERSION  
I31503.1 GI:1822294  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 30)  
AUTHORS  
Weber, J.L.  
TITLE  
Length polymorphisms in (dc-da).sub.n.(ag-dt).sub.n sequences and method of using the same  
JOURNAL  
Patent: US 5582979-A 415 10-DEC-1996;  
FEATURES  
Location/Qualifiers  
1..30  
Source  
/organism="unknown"  
BASE COUNT  
15 a 13 c 2 g 0 t  
ORIGIN  
Query Match  
Best Local Similarity 0.6%; Score 30; DB 6; Length 30;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2310 CACACACACACACACACACACACACACACA 2339  
|||||  
Db 1 CACACACACACACACACACACACACACACA 30  
RESULT 19  
AR007294  
LOCUS  
DEFINITION  
Accession  
AR007294  
VERSION  
AR007294.1 GI:3966778  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 28)  
AUTHORS  
Thompson, J.D. and Draper, K.G.  
TITLE  
Method and reagent for treatment of diseases caused by expression of the bcl-2 gene  
JOURNAL  
Patent: US 5750390-A 8 12-MAY-1998;  
FEATURES  
Location/Qualifiers  
1..28  
Source  
/organism="unknown"  
BASE COUNT  
3 a 13 c 7 g 5 t  
ORIGIN

Query Match 0.6%; Score 28; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 3

RESULT 21

A56844/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Query Match 0.6%; Score 28; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 3

RESULT 21

A56844/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Query Match 0.6%; Score 28; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 3

RESULT 21

A56844/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Query Match 0.6%; Score 28; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CCTGTGTCACCTGGCCCTCGCCAAAS 1756

Db 1 CCTGTGTCACCTGGCCCTCGCCAAAG 28

RESULT 20

A56841/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 4504

CTTCAGGGTCTTCTGAAATGCAGTGGT 4531

Db 30

CTTCAGGGTCTTCTGAAATGCAGTGGT 3

RESULT 21

A56844/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

[illegible]









[illegible]







c 83	26.8	0.5	38	24	ABK24299	Human microsatelli	c 156	23.8	0.5	27	13	AAO34181	Microsatellite seq
c 84	26.8	0.5	39	13	AAQ33648	Microsatellite seq	c 157	23.8	0.5	27	13	AAQ33678	Microsatellite seq
c 85	26.8	0.5	39	13	AAQ33807	Microsatellite seq	c 158	23.8	0.5	27	13	AAQ33804	Microsatellite seq
c 86	26.8	0.5	39	13	AAQ33825	Microsatellite seq	c 159	23.8	0.5	27	16	AAQ83951	Oligonucleotide cl
c 87	26.8	0.5	39	13	AAQ33971	Microsatellite seq	c 160	23.8	0.5	27	18	AAAT65733	Repeat sequence fr
c 88	26.8	0.5	39	18	AAAT65731	Repeat sequence fr	c 161	23.8	0.5	27	22	AAH24300	Synthetic antineop
c 89	26.8	0.5	39	18	AAAT65714	Repeat sequence fr	c 162	23.8	0.5	27	22	AAH45303	Human Bcl-2 mutage
c 90	26.8	0.5	40	13	AAQ34091	Sequence of a micr	c 163	23.8	0.5	27	22	AAH45305	Human Bcl-2 mutage
c 91	26.8	0.5	40	18	AAAT65725	Repeat sequence fr	c 164	23.8	0.5	27	22	AAH45306	Human Bcl-2 mutage
c 92	26.8	0.5	40	18	AAAT66051	(dC-dA)n.(dG-dT)n	c 165	23.8	0.5	27	22	AAH46001	Synthetic oligonuc
c 93	26.4	0.5	38	13	AAQ33843	Microsatellite seq	c 166	23.8	0.5	27	22	AAH46005	Synthetic oligonuc
c 94	26.4	0.5	36	13	AAQ34107	Sequence of a micr	c 167	23.8	0.5	27	22	AAH46017	Synthetic oligonuc
c 95	26.2	0.5	29	21	AAAC65050	Human bcl genes an	c 168	23.8	0.5	27	22	AAH460473	Oligonucleotide cl
c 96	26.2	0.5	40	18	AAAT65736	Repeat sequence fr	c 169	23.8	0.5	36	16	AAO83935	Oligonucleotide cl
c 97	26	0.5	34	13	AAQ33734	Microsatellite seq	c 170	23.6	0.5	33	13	AAQ33944	Microsatellite seq
c 98	25.8	0.5	29	13	AAQ33687	Microsatellite seq	c 171	23.6	0.5	37	13	AAQ33698	Microsatellite seq
c 99	25.8	0.5	29	13	AAQ33846	Microsatellite seq	c 172	23.6	0.5	38	13	AAQ33767	Microsatellite seq
c 100	25.8	0.5	29	13	AAQ33956	Microsatellite seq	c 173	23.2	0.5	28	13	AAQ34074	Microsatellite seq
c 101	25.8	0.5	29	13	AAQ33977	Microsatellite seq	c 174	23.2	0.5	28	13	AAQ33933	Microsatellite seq
c 102	25.8	0.5	29	16	AAQ83953	Oligonucleotide cl	c 175	23.2	0.5	28	13	AAQ33630	Microsatellite seq
c 103	25.8	0.5	29	18	AAAT65712	Repeat sequence fr	c 176	23.2	0.5	32	13	AAQ34149	Sequence of a micr
c 104	25.8	0.5	29	18	AAAT65760	Repeat sequence fr	c 177	23.2	0.5	37	13	AAQ34184	Microsatellite seq
c 105	25.8	0.5	29	22	AAAF60474	Oligonucleotide cl	c 178	23	0.5	23	14	AAQ51950	Bcl-2 mRNA ribozym
c 106	25.8	0.5	30	18	AAAT65789	Repeat sequence fr	c 179	23	0.5	23	21	AAA26253	Bcl-2 antisense ol
c 107	25.8	0.5	30	23	AAAS13787	Simple sequence re	c 180	23	0.5	23	21	AAA26255	Bcl-2 antisense ol
c 108	25.8	0.5	30	24	AAAL42354	Novel sand pear mi	c 181	23	0.5	36	17	AAAT35026	Triplex-forming ol
c 109	25.8	0.5	39	18	AAAT65775	Repeat sequence fr	c 182	22.8	0.4	26	13	AAQ34083	Microsatellite seq
c 110	25.4	0.5	27	22	AAH45300	Human Bcl-2 mutage	c 183	22.8	0.4	26	13	AAQ33684	Microsatellite seq
c 111	25.4	0.5	27	22	AAH45302	Human Bcl-2 mutage	c 184	22.8	0.4	26	13	AAQ33704	Microsatellite seq
c 112	25.4	0.5	35	13	AAQ33695	Microsatellite seq	c 185	22.8	0.4	26	13	AAQ33831	Microsatellite seq
c 113	25.2	0.5	32	13	AAQ34119	Microsatellite seq	c 186	22.8	0.4	26	13	AAQ33837	Microsatellite seq
c 114	25.2	0.5	32	18	AAAT66057	Sequence of a micr	c 187	22.8	0.4	26	22	AAI64469	SSR motif #19. Un
c 115	25.2	0.5	37	13	AAQ33669	(dC-dA)n.(dG-dT)n	c 188	22.6	0.4	40	21	AAAT96060	Polynucleotide seq
c 116	25	0.5	25	13	AAQ22742	Microsatellite seq	c 189	22.4	0.4	24	17	AAAT36054	bcl-2 reverse PCR
c 117	25	0.5	25	21	AAAT73296	Primer bcl-2 adjac	c 190	22.4	0.4	24	20	AAAT36250	Reverse primer for
c 118	25	0.5	25	21	AAAT73297	Bcl-2 specific gen	c 191	22.4	0.4	24	20	AAAT81830	Mouse bcl-2 revers
c 119	24.8	0.5	28	13	AAQ34027	Microsatellite seq	c 192	22.4	0.4	24	21	AAAT88587	PCR primer for mou
c 120	24.8	0.5	28	13	AAQ34035	Microsatellite seq	c 193	22.4	0.4	24	21	AAAT89800	Reverse primer for
c 121	24.8	0.5	28	13	AAQ34161	Sequence of a micr	c 194	22.4	0.4	24	21	AAAT88011	Mouse bcl-2 revers
c 122	24.8	0.5	28	13	AAQ33645	Microsatellite seq	c 195	22.4	0.4	24	22	AAAT92685	Human Bcl-2 PCR pr
c 123	24.8	0.5	28	18	AAAT66102	Repeat sequence fo	c 196	22.4	0.4	26	22	AAAT92621	Bcl-2 antisense ol
c 124	24.8	0.5	28	23	AAAS13711	Simple sequence re	c 197	22.4	0.4	40	24	ABK94443	Human BRCAL/hMLH1
c 125	24.6	0.5	40	13	AAQ25030	Oligonucleotide sp	c 198	22.2	0.4	27	13	AAQ34077	Microsatellite seq
c 126	24.4	0.5	34	14	AAQ36324	NGFR target sequen	c 199	22.2	0.4	27	22	AAH45298	Human Bcl-2 mutage
c 127	24.2	0.5	30	21	AAAT98502	H. discus derived	c 200	22.2	0.4	27	22	AAH45301	Human Bcl-2 mutage
c 128	24.2	0.5	33	13	AAQ33731	Microsatellite seq	c 201	22.2	0.4	27	22	AAH45304	Human Bcl-2 mutage
c 129	24.2	0.5	37	13	AAQ33710	Microsatellite seq	c 202	22.2	0.4	22	14	AAQ49816	Bcl-2 antisense ol
c 130	24	0.5	24	13	AAQ30093	MBR primer for Maj	c 203	22	0.4	22	14	AAQ49817	Bcl-2 antisense ol
c 131	24	0.5	24	16	AAQ86624	Bcl-2 chromosomal	c 204	22	0.4	22	14	AAQ51952	Bcl-2 antisense ol
c 132	24	0.5	24	16	AAQ86625	Bcl-2 chromosomal	c 205	22	0.4	22	16	AAAT01266	Bcl-2 mRNA ribozym
c 133	24	0.5	24	17	AAAT42415	Bcl-2 t(14;18) pro	c 206	22	0.4	22	16	AAAT01267	bcl-2 gene specifi
c 134	24	0.5	24	17	AAAT42416	Bcl-2 t(14;18) pro	c 207	22	0.4	22	17	AAAT17218	bcl-2 gene specifi
c 135	24	0.5	24	17	AAAT15569	Bcl-2 chromosomal	c 208	22	0.4	22	21	AAAT65038	Target primer 3 fo
c 136	24	0.5	24	17	AAAT15570	Bcl-2 chromosomal	c 209	22	0.4	22	21	AAAT65038	Bcl2 RNA Rn-PCR pr
c 137	24	0.5	24	19	AAAT66348	Bcl-2 chromosomal	c 210	22	0.4	30	18	AAAT79848	Human bcl-2 gene n
c 138	24	0.5	24	19	AAAT66347	Bcl-2 chromosomal	c 211	22	0.4	30	18	AAAT79848	PCR primer 2 used
c 139	24	0.5	24	20	AAAT23189	Bcl-2 t(14;18) pro	c 212	22	0.4	33	18	AAAT65770	Repeat sequence fr
c 140	24	0.5	24	20	AAAT23190	Bcl-2 t(14;18) pro	c 213	21.8	0.4	35	13	AAQ34021	Microsatellite seq
c 141	24	0.5	24	21	AAAT76092	Bcl-2 PCR primer #	c 214	21.8	0.4	25	13	AAQ33642	Microsatellite seq
c 142	24	0.5	24	22	AAAT12909	PCR primer PAL for	c 215	21.8	0.4	25	13	AAQ33962	Microsatellite seq
c 143	24	0.5	24	22	AAAT82684	Human Bcl-2 PCR pr	c 216	21.8	0.4	25	13	AAQ33918	Microsatellite seq
c 144	24	0.5	24	24	ABN85362	Bcl-2 related olig	c 217	21.8	0.4	25	18	AAAT65734	Repeat sequence fr
c 145	24	0.5	24	24	ABN852487	Fluorescent probe	c 218	21.8	0.4	25	22	AAAT65734	SNP specific SNPE
c 146	24	0.5	24	24	ABN88835	Human bcl-2 PCR pr	c 219	21.8	0.4	26	14	AAAT47179	MHC DR A intron bi
c 147	24	0.5	24	24	ABK15646	Bcl-2 RNA-DNA hybr	c 220	21.8	0.4	28	18	AAAT79847	Human bcl-2 gene n
c 148	24	0.5	24	24	ABK15648	Bcl-2 RNA-DNA hybr	c 221	21.8	0.4	33	18	AAAT96579	Mouse bcl-w gene p
c 149	24	0.5	32	22	AAH45308	Human Bcl-2 PCR pr	c 222	21.6	0.4	31	21	AAAT50360	Bcl2 gene 3' PCR p
c 150	24	0.5	36	16	AAO86648	Bcl-2 splice accep	c 223	21.6	0.4	34	13	AAQ33924	Microsatellite seq
c 151	24	0.5	36	19	AAAT19656	Human bcl-2 oligon	c 224	21.4	0.4	33	15	AAQ73441	Crohn's disease/ul
c 152	24	0.5	36	24	ABL54154	Bcl-2 antisense ol	c 225	21.2	0.4	27	13	AAQ33740	Microsatellite seq
c 153	23.8	0.5	27	13	AAQ34012	Microsatellite seq	c 226	21.2	0.4	28	14	AAAT46987	First type III-C a
c 154	23.8	0.5	27	13	AAQ34044	Microsatellite seq	c 227	21.2	0.4	28	18	AAAT71141	Fibronectin fragme
c 155	23.8	0.5	27	13	AAQ34143	Sequence of a micr	c 228	21.2	0.4	28	19	AAAT28773	Fibronectin PCR 3'

c 229	21.2	0.4	28	20	AAV69809	Human fibronectin	302	20	0.4	20	22	AA15638	Human Bcl-2 protei
c 230	21.2	0.4	33	22	AAH77493	Human zinc finger	303	20	0.4	20	22	AA15639	Human Bcl-2 protei
c 231	21	0.4	21	24	ABN85360	Bcl-2 related olig	304	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 232	21	0.4	21	24	ABN85361	Bcl-2 related olig	305	20	0.4	20	22	AA15641	Human Bcl-2 protei
c 233	21	0.4	31	18	AA196580	Mouse bcl-w gene p	306	20	0.4	20	22	AA15642	Human Bcl-2 protei
c 234	21	0.4	31	18	AA196580	Rat serotonin regi	307	20	0.4	20	22	AA15643	Human Bcl-2 protei
c 235	21	0.4	33	14	AAQ41697	Normalised library	308	20	0.4	20	22	AA15646	Human Bcl-2 protei
c 236	21	0.4	35	16	AAQ87895	Normalised library	309	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 237	21	0.4	35	16	AAQ87896	Human reproductiv	310	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 238	21	0.4	38	22	AA107487	Sequence of a micr	311	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 239	20.8	0.4	40	13	AAQ34094	Microsatellite seq	312	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 240	20.8	0.4	24	13	AAQ34024	Microsatellite seq	313	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 241	20.8	0.4	24	13	AAQ34065	Microsatellite seq	314	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 242	20.8	0.4	24	13	AAQ33707	Sequence of a micr	315	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 243	20.8	0.4	24	13	AAQ33986	Microsatellite seq	316	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 244	20.8	0.4	24	13	AAQ33909	Microsatellite seq	317	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 245	20.8	0.4	24	16	AA162762	Murine bcl-2 rever	318	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 246	20.8	0.4	24	18	AA166096	Repeat sequence fo	319	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 247	20.8	0.4	24	22	AAH46015	Synthetic oligonuc	320	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 248	20.8	0.4	24	22	AAH46016	Synthetic oligonuc	321	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 249	20.8	0.4	24	22	AAH46016	Immunostimulatory	322	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 250	20.8	0.4	24	22	AAH46016	SSR motif #17. Un	323	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 251	20.8	0.4	24	22	AAH40163	SNP specific SNPE	324	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 252	20.8	0.4	25	22	AAH27907	Compound in phase	325	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 253	20.8	0.4	40	17	AA17907	PCR primer used to	326	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 254	20.6	0.4	40	24	AA17907	Human Bcl-2 forwa	327	20	0.4	20	22	AA15640	Human Bcl-2 protei
c 255	20.6	0.4	27	17	AA18388	Human ASTH1 5' re	328	19.8	0.4	28	15	AAQ70677	Hepatitis C virus
c 256	20.6	0.4	36	21	AAH80358	Triplex-forming ol	329	19.8	0.4	28	19	AAQ70677	Microsatellite seq
c 257	20.6	0.4	37	21	AAH35027	Murine renal compe	330	19.8	0.4	28	19	AAQ70677	Microsatellite seq
c 258	20.6	0.4	39	24	AAH96052	Rat histamine H4 r	331	19.8	0.4	28	19	AAQ70677	Repeat sequence fo
c 259	20.4	0.4	39	21	AAH70998	Bcl2 RNA RT-PCR pr	332	19.8	0.4	28	19	AAQ70677	Oligonucleotide cl
c 260	20.4	0.4	31	22	AAH65039	Human single nucle	333	19.8	0.4	28	19	AAQ70677	SNP specific SNPE
c 261	20.4	0.4	31	22	AAH31038	Diabody mutagenesi	334	19.8	0.4	28	19	AAQ70677	Purine rich HER-2
c 262	20.4	0.4	34	15	AAH68340	MAB GAH gene prime	335	19.8	0.4	28	19	AAQ70677	Her-2/neu promoter
c 263	20.4	0.4	37	14	AAH33029	Corneodesmosin sin	336	19.8	0.4	28	19	AAQ70677	GA-rich triplex bi
c 264	20.4	0.4	37	22	AAH14353	Human manganese su	337	19.8	0.4	28	19	AAQ70677	C/EBP-beta antisen
c 265	20.2	0.4	38	22	AAH14353	Target sequence #8	338	19.8	0.4	31	16	AAQ88044	Human C/EBP polynu
c 266	20.2	0.4	26	14	AAH44016	SSA primer 2 for a	339	19.8	0.4	34	21	AAH20580	Human adenosine re
c 267	20.2	0.4	32	24	AAH89470	Human p70 ribosome	340	19.8	0.4	34	21	AAH20580	C/EBP-beta antisen
c 268	20.2	0.4	32	24	AAH89470	SPX2S oligonucleo	341	19.8	0.4	35	20	AAH20580	Human C/EBP polynu
c 269	20.2	0.4	38	12	AAH13203	Polynucleotide seq	342	19.8	0.4	35	21	AAH20580	Human adenosine re
c 270	20	0.4	40	21	AAH296043	Primer for major b	343	19.8	0.4	36	20	AAH20580	C/EBP-beta antisen
c 271	20	0.4	40	21	AAH63253	Bcl-2 translation	344	19.8	0.4	36	21	AAH20580	Human adenosine re
c 272	20	0.4	20	16	AAH86649	Bcl-2 chromosomal	345	19.8	0.4	37	21	AAH20580	C/EBP-beta antisen
c 273	20	0.4	20	16	AAH86649	Human BCL2 cDNA se	346	19.8	0.4	37	21	AAH20580	Human adenosine re
c 274	20	0.4	20	17	AAH33696	Human BCL2 cDNA an	347	19.8	0.4	37	21	AAH20580	C/EBP-beta antisen
c 275	20	0.4	20	17	AAH33696	BCL-2 chromosomal	348	19.8	0.4	37	21	AAH20580	Human adenosine re
c 276	20	0.4	20	17	AAH33696	BCL-2 chromosomal	349	19.8	0.4	37	21	AAH20580	C/EBP-beta antisen
c 277	20	0.4	20	18	AAH15568	Human bcl-2 oncoge	350	19.8	0.4	38	20	AAH20580	Human adenosine re
c 278	20	0.4	20	18	AAH15568	Human bcl-2 oncoge	351	19.8	0.4	38	20	AAH20580	C/EBP-beta antisen
c 279	20	0.4	20	18	AAH15568	Primer for detecti	352	19.8	0.4	38	21	AAH20580	Human adenosine re
c 280	20	0.4	20	18	AAH15568	Primer for bcl-2 a	353	19.8	0.4	39	21	AAH20580	Human adenosine re
c 281	20	0.4	20	19	AAH66346	BCL-2 chromosomal	354	19.8	0.4	39	21	AAH20580	C/EBP-beta antisen
c 282	20	0.4	20	19	AAH66346	Human bcl-2 antise	355	19.8	0.4	40	21	AAH20580	Human adenosine re
c 283	20	0.4	20	19	AAH66346	Human bcl-2 transc	356	19.8	0.4	40	21	AAH20580	C/EBP-beta antisen
c 284	20	0.4	20	20	AAH23188	BCL-2 t(14;18) pri	357	19.8	0.4	40	21	AAH20580	Human adenosine re
c 285	20	0.4	20	20	AAH27537	Synthetic RNA sequ	358	19.8	0.4	40	21	AAH20580	Polynucleotide seq
c 286	20	0.4	20	20	AAH27537	Antisense oligonuc	359	19.8	0.4	40	21	AAH20580	Polymorphism detec
c 287	20	0.4	20	20	AAH27537	Antisense oligonuc	360	19.8	0.4	40	21	AAH20580	Human bcl genes an
c 288	20	0.4	20	20	AAH27537	Antisense oligonuc	361	19.8	0.4	40	21	AAH20580	SSR motif #20. Un
c 289	20	0.4	20	20	AAH27537	PCR primer for hum	362	19.8	0.4	40	21	AAH20580	Oligonucleotide fo
c 290	20	0.4	20	21	AAH27537	PCR primer for hum	363	19.8	0.4	40	21	AAH20580	HSV-1 exon 3 of IR
c 291	20	0.4	20	21	AAH27537	Human Bcl-2 mRNA t	364	19.8	0.4	40	21	AAH20580	Antibody heavy cha
c 292	20	0.4	20	22	AAH15627	Human Bcl-2 protei	365	19.8	0.4	40	21	AAH20580	Anti-A33 antigen a
c 293	20	0.4	20	22	AAH15627	Human Bcl-2 protei	366	19.8	0.4	40	21	AAH20580	Rabbit VH and huma
c 294	20	0.4	20	22	AAH15627	Human Bcl-2 protei	367	19.8	0.4	40	21	AAH20580	PCR primer used fo
c 295	20	0.4	20	22	AAH15627	Human Bcl-2 protei	368	19.8	0.4	40	21	AAH20580	Murine bcl-2 forw
c 296	20	0.4	20	22	AAH15627	Human Bcl-2 protei	369	19.8	0.4	40	21	AAH20580	Phosphodiester oli
c 297	20	0.4	20	22	AAH15627	Human Bcl-2 protei	370	19.8	0.4	40	21	AAH20580	Herpes Simplex Vir
c 298	20	0.4	20	22	AAH15627	Human Bcl-2 protei	371	19.8	0.4	40	21	AAH20580	Herpes Simplex Vir
c 299	20	0.4	20	22	AAH15627	Human Bcl-2 protei	372	19.8	0.4	40	21	AAH20580	Primer 5WK for IgE
c 300	20	0.4	20	22	AAH15627	Human Bcl-2 protei	373	19.8	0.4	40	21	AAH20580	Phosphorothioate s
c 301	20	0.4	20	22	AAH15627	Human Bcl-2 protei	374	19.8	0.4	40	21	AAH20580	

375	19.4	0.4	0.4	32	16	AAQ87894	Normalised library	448	19	0.4	39	18	AAQ64939	Antisense primer S
376	19.4	0.4	0.4	32	20	AAQ55013	C/EBP-beta antisen	c 449	19	0.4	39	18	AAQ65775	Repeat sequence fr
377	19.4	0.4	0.4	32	21	AAQ20582	Human C/EBP polyu	c 450	19	0.4	39	20	AAQ87088	DNA ligand T39 to
378	19.4	0.4	0.4	32	21	AAQ34460	Human adenosine re	c 451	19	0.4	39	22	AAQ21660	Immunoglobulin tra
379	19.4	0.4	0.4	32	21	AAQ98509	H. discus derived	c 452	19	0.4	40	21	AAQ05334	PCR primer bMm220r
380	19.4	0.4	0.4	33	20	AAQ55012	C/EBP-beta antisen	c 453	19	0.4	40	21	AAQ96163	Polynucleotide seq
381	19.4	0.4	0.4	33	21	AAQ20581	Human C/EBP polyu	c 454	19	0.4	40	21	AAQ43349	Murine Tyrp-1 gene
382	19.4	0.4	0.4	33	21	AAQ34459	Human adenosine re	c 455	19	0.4	40	22	AAQ20350	HHV6 virus p41 gen
383	19.4	0.4	0.4	33	22	AAQ28309	3' untranslated re	c 456	19	0.4	40	22	AAQ20354	HHV6 virus p41 gen
384	19.4	0.4	0.4	33	24	AAQ96737	Human phosphatidyl	c 457	19	0.4	40	24	AAQ38855	Human GFATL1, PCR p
385	19.4	0.4	0.4	35	16	AAQ87901	Normalised library	c 458	19	0.4	40	24	AAQ22107	Oligonucleotide 40
386	19.4	0.4	0.4	35	16	AAQ87898	Human PDE1A1 3' UT	c 459	18.8	0.4	40	24	AAQ34038	Microsatellite seq
387	19.4	0.4	0.4	36	24	AAQ33387	Human PDE1A1 3' UT	c 460	18.8	0.4	22	13	AAQ34038	Microsatellite seq
388	19.4	0.4	0.4	38	12	AAQ14795	Hepatitis C diagno	c 461	18.8	0.4	22	13	AAQ33675	Microsatellite seq
389	19.4	0.4	0.4	40	21	AAQ03676	Polynucleotide seq	c 462	18.8	0.4	22	13	AAQ33810	Microsatellite seq
390	19.4	0.4	0.4	40	21	AAQ96047	Polynucleotide seq	c 463	18.8	0.4	22	13	AAQ33991	Microsatellite seq
391	19.4	0.4	0.4	40	21	AAQ26165	Quadruplex DNA seq	c 464	18.8	0.4	22	16	AAQ83952	Oligonucleotide cl
392	19.4	0.4	0.4	40	22	AAQ57137	HHV6 virus p41 gen	c 465	18.8	0.4	22	18	AAQ65727	Repeat sequence fr
393	19.4	0.4	0.4	40	22	AAQ20347	Human bcl genes an	c 466	18.8	0.4	22	22	AAQ16448	SSR motif #8. Uni
394	18.2	0.4	0.4	20	21	AAQ65053	MC0677, a competit	c 467	18.8	0.4	22	22	AAQ16448	SSR motif #18. Uni
395	19.2	0.4	0.4	24	18	AAQ99279	Nucleotide sequenc	c 468	18.8	0.4	23	22	AAQ39005	SNP specific upper
396	19.2	0.4	0.4	24	19	AAQ31736	Oligonucleotide MC	c 469	18.8	0.4	24	18	AAQ99284	MC0677, a competit
397	19.2	0.4	0.4	24	20	AAQ04079	PCR primer specifl	c 470	18.8	0.4	24	19	AAQ31741	Nucleotide sequenc
398	19.2	0.4	0.4	24	21	AAQ60156	Maize root transcr	c 471	18.8	0.4	24	24	AAQ04084	Oligonucleotide MJ
399	19.2	0.4	0.4	27	22	AAQ76445	Maize root transcr	c 472	18.8	0.4	24	24	AAQ04084	SNP specific lower
400	19.2	0.4	0.4	27	22	AAQ76448	Maize root transcr	c 473	18.8	0.4	25	15	AAQ55856	Probe for Fragile
401	18.2	0.4	0.4	27	22	AAQ26309	Triplex-forming ol	c 474	18.8	0.4	25	16	AAQ85271	Fragile X probe.
402	19.2	0.4	0.4	28	19	AAQ44665	Primer JWTCR202 us	c 475	18.8	0.4	25	16	AAQ55267	Chicken insulator
403	19.2	0.4	0.4	32	19	AAQ54297	Soluble sc-TCR fus	c 476	18.8	0.4	25	20	AAQ05155	Human EPIL/placent
404	19.2	0.4	0.4	32	20	AAQ53379	Antitumoural phosph	c 477	18.8	0.4	27	21	AAQ89469	Human gene signatu
405	19.2	0.4	0.4	34	18	AAQ93827	Reverse PCR primer	c 478	18.8	0.4	31	23	AAQ06380	Human inflammatory
406	19.2	0.4	0.4	35	16	AAQ87899	Normalised library	c 479	18.8	0.4	32	14	AAQ52007	RNA template, AU u
407	19.2	0.4	0.4	35	16	AAQ87905	Normalised library	c 480	18.8	0.4	32	21	AAQ52007	5' PCR primer ipt
408	19.2	0.4	0.4	35	18	AAQ3816	Antitumoural phosph	c 481	18.8	0.4	32	22	AAQ164452	RNA template, (AU)
409	19.2	0.4	0.4	36	18	AAQ43757	TNFRI cytoplasmic	c 482	18.8	0.4	33	22	AAQ67673	Human c-myc hamme
410	19.2	0.4	0.4	37	22	AAQ91070	Human inflammatory	c 483	18.8	0.4	35	17	AAQ10277	PCR primer 2-BST-5
411	19.2	0.4	0.4	37	22	AAQ85682	Pea blight resista	c 484	18.8	0.4	36	16	AAQ25542	PCR primer used to
412	19.2	0.4	0.4	37	22	AAQ85682	Cdn primer Bclx 2-	c 485	18.8	0.4	36	22	AAQ91407	Polynucleotide seq
413	19.2	0.4	0.4	39	16	AAQ85496	Primer JSS33(B) us	c 486	18.8	0.4	36	24	AAQ27117	Mutagenic primer A
414	19.2	0.4	0.4	39	21	AAQ34974	BCG deletion regio	c 487	18.8	0.4	37	21	AAQ00622	Immunoglobulin tra
415	19.2	0.4	0.4	40	17	AAQ33546	Polynucleotide seq	c 488	18.8	0.4	37	24	AAQ27124	Zeta globin primer
416	19.2	0.4	0.4	40	22	AAQ26152	HHV6 virus p41 gen	c 489	18.8	0.4	37	24	AAQ27125	Human GDMPLP-1 25-m
417	19.2	0.4	0.4	40	22	AAQ20339	BCL-2 mRNA ribozym	c 490	18.8	0.4	38	17	AAQ81930	Target sequence fo
418	19	0.4	0.4	41	14	AAQ51947	BCL-2 mRNA ribozym	c 491	18.8	0.4	38	17	AAQ81930	Murine Zif(C7)6-Ju
419	19	0.4	0.4	41	14	AAQ51957	BCL-2 mRNA ribozym	c 492	18.8	0.4	40	19	AAQ08781	supf gene triplex
420	19	0.4	0.4	41	14	AAQ51958	BCL-2 mRNA ribozym	c 493	18.8	0.4	40	20	AAQ86733	
421	19	0.4	0.4	41	14	AAQ51960	BCL-2 mRNA ribozym	c 494	18.8	0.4	40	21	AAQ29815	
422	19	0.4	0.4	41	15	AAQ63256	Probe for major br	c 495	18.8	0.4	40	21	AAQ29815	
423	19	0.4	0.4	41	18	AAQ91695	Human bcl-2 oncoge	c 496	18.8	0.4	40	22	AAQ21661	
424	19	0.4	0.4	42	19	AAQ206730	Antisense oligomer	c 497	18.8	0.4	40	22	AAQ31425	
425	19	0.4	0.4	42	19	AAQ95740	PKCalpha primer-pa	c 498	18.6	0.4	25	24	ABN03891	
426	19	0.4	0.4	42	19	AAQ88834	Human bcl-2 PCR pr	c 499	18.6	0.4	28	20	AAQ03258	
427	19	0.4	0.4	42	20	AAQ15645	Human bcl-2 protei	c 500	18.6	0.4	28	22	AAQ06063	
428	19	0.4	0.4	42	20	AAQ80380	PCR primer for ost	c 500	18.6	0.4	30	16	AAQ81071	
429	19	0.4	0.4	42	22	AAQ45299	Human Bcl-2 mutag							
430	19	0.4	0.4	43	30	AAQ46078	Human G protein co							
431	19	0.4	0.4	43	30	AAQ03856	Human XRC3 gene P							
432	19	0.4	0.4	43	32	AAQ27960	PCR primer for Sug							
433	19	0.4	0.4	43	32	AAQ73995	Sugarcane bacillif							
434	19	0.4	0.4	43	32	AAQ739514	ScBV gene amplifly							
435	19	0.4	0.4	43	35	AAQ99571	Immunostimulatory							
436	19	0.4	0.4	43	35	AAQ38795	Immunostimulatory							
437	19	0.4	0.4	43	36	AAQ95743	PKCalpha primer-pa							
438	19	0.4	0.4	43	37	AAQ74326	Lobolly pine SSR							
439	19	0.4	0.4	43	38	AAQ98404	Truncated SELEX de							
440	19	0.4	0.4	43	38	AAQ86654	Spectroscopically							
441	19	0.4	0.4	43	38	AAQ38802	Thrombin ligand fo							
442	19	0.4	0.4	43	38	AAQ85812	Thrombin-binding n							
443	19	0.4	0.4	43	38	AAQ80049	Thrombin binding l							
444	19	0.4	0.4	43	38	AAQ243894	M. tuberculosis rp							
445	19	0.4	0.4	43	38	AAQ70817	Thrombin high affi							
446	19	0.4	0.4	43	39	AAQ90410	S. lividans xylana							
447	19	0.4	0.4	43	39	AAQ18644	Probe (S. lividans							

## ALIGNMENTS

## RESULT 1

AAQ51948  
ID AAQ51948 standard; RNA; 37 BP.

XX AAQ51948;

AC AAQ51948;

XX 26-MAY-1994 (first entry)

XX BCL-2 mRNA ribozyme cleavable nucleotide (1415).

DE Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;

XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;

KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;

KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;

KW human; chronic myelogenous leukemia; CML; follicular lymphoma;





AAQ51966

2000

Synthetic.

PR 10-NOV-2000; 2000US-0709170.

PR 10-NOV-2000; 2000US-0709170.

PA (GENT-) GENTA INC.  
 PI Warrel RP, Klem RE, Fingert H;  
 XX WPI; 2002-371796/40.  
 DR  
 XX  
 XX Treating or preventing cancer, tumors and carcinomas, comprises  
 PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
 PT high doses for short period for time with one or more cancer  
 PT therapeutics -  
 XX  
 XX Disclosure; Page 53; 64pp; English.  
 PS  
 XX  
 CC The present sequence is that of a B cell lymphoma/leukemia-2  
 CC (bcl-2) antisense oligonucleotide. The present invention is  
 CC directed to the use of bcl-2 antisense oligomers, particularly  
 CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.  
 CC Administration at high doses results in significant therapeutic  
 CC responses, including low toxicity, high tolerance and prolonged  
 CC survival. Administration at high doses for short periods of time  
 CC (less than 14 days) also provides significant therapeutic responses  
 CC in the treatment of cancer. The bcl-2 antisense oligomer may also  
 CC be used to increase the sensitivity of a subject to cancer  
 CC therapeutics, and in combination with hormone treatment or gene  
 CC therapy. Conditions that may be treated or prevented include  
 CC cancer of the hematopoietic system, skin, bone and soft tissue,  
 CC reproductive system, genitourinary system, breast, endocrine  
 CC system, brain, central nervous system, peripheral nervous system,  
 CC kidney, lung, respiratory system, thorax, gastrointestinal and  
 CC alimentary canal, lymph nodes, pancreas, hepatobiliary system, or  
 CC cancer of unknown primary site, non-Hodgkin's lymphoma, Hodgkin's  
 CC lymphoma, leukemia, colon carcinoma, rectal carcinoma, pancreatic,  
 CC breast, ovarian, prostate, cervical, testicular, head and neck or  
 CC brain cancer, renal cell carcinoma, hepatoma, bile duct carcinoma,  
 CC choriocarcinoma, lung carcinoma, bladder carcinoma and melanoma  
 CC (all claimed).  
 XX  
 XX Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;  
 SQ  
 Query Match 0.7%; Score 35; DB 24; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1442 CTTTTCCTCTGGAGGATGGCGACGCTGGGAGA 1476  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 CTTTTCCTCTGGAGGATGGCGACGCTGGGAGA 35  
 RESULT 8  
 AAQ51962  
 ID AAQ51962 standard; RNA; 34 BP.  
 XX  
 XX AAQ51962;  
 XX  
 XX 26-MAY-1994 (first entry)  
 DT  
 XX  
 XX BCL-2 mRNA ribozyme cleavable nucleotide (2043).  
 DE  
 XX  
 KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
 KW hairpin; hepatitis delta virus; group I intron; RNasep; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09323057-A.  
 PN  
 XX  
 XX 25-NOV-1993.  
 PD  
 XX

PF 13-MAY-1993; 93WO-US04573.  
 XX  
 XX 14-MAY-1992; 92US-0882822.  
 PR 14-MAY-1992; 92US-0882885.  
 PR 26-AUG-1992; 92US-0936110.  
 PR 26-AUG-1992; 92US-0936421.  
 PR 26-AUG-1992; 92US-0936422.  
 PR 26-AUG-1992; 92US-0936531.  
 PR 26-AUG-1992; 92US-0936532.  
 PR 07-DEC-1992; 92US-0987131.  
 PR 19-JAN-1993; 93US-0006122.  
 PR 19-JAN-1993; 93US-0008910.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Draper KG, Thompson JD;  
 PI  
 XX WPI; 1993-386203/48.  
 DR  
 XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA  
 XX associated with tumors or mRNA expressed from gene encoding  
 XX multiple drug resistance  
 PT  
 XX Claim 3; Fig 6; 69pp; English.  
 PS  
 XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
 CC associated with development or maintenance of chronic myelogenous  
 CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or  
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute  
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma  
 CC and lung cancer. The full length mRNAs containing these target  
 CC sequences, encode aberrant cellular proteins which are able to control  
 CC cellular proliferation and are directly linked to a leukemic  
 CC phenotype. These target sequences are identified by the ribozyme of  
 CC the invention. The ribozymes is formed in a hammerhead motif, but may  
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group  
 CC I intron or RNasep-like RNA. These ribozymes may be used to inhibit  
 CC the development or expression of a transformed phenotype in man and  
 CC other animals by modulating expression of the corresponding gene.  
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed  
 CC cells elicits inhibition of the transformed state. Multiple drug  
 CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of  
 CC drug resistance used by transformed cells and thus enhances drug  
 CC therapies for tumors. The ribozymes may also be used to study  
 CC genetic drift and mutations within cells.  
 XX  
 XX Sequence 34 BP; 6 A; 9 C; 11 G; 8 U; 0 other;  
 SQ  
 Query Match 0.7%; Score 34; DB 14; Length 34;  
 Best Local Similarity 76.5%; Pred. No. 5.2e+02;  
 Matches 26; Conservative 8; Mismatches 0; Indels 0; Gaps 0;  
 OY 2043 GGATGCCCTTTGTGGAACTGTACGGCCCCCAGCATG 2076  
 |||:||||:||||:||||:||||:||||:|  
 DB 1 GGAUGCCUUUGUGGAACUGACGGCCCCCAGCAUG 34  
 RESULT 9  
 AAQ51967  
 ID AAQ51967 standard; RNA; 34 BP.  
 XX  
 XX AAQ51967;  
 AC  
 XX  
 XX 26-MAY-1994 (first entry)  
 DT  
 XX  
 XX BCL-2 mRNA ribozyme cleavable nucleotide (2235).  
 DE  
 XX  
 KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
 KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
 KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
 KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
 KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
 KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
 KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
 KW hairpin; hepatitis delta virus; group I intron; RNasep; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W09323057-A.  
 PN  
 XX  
 XX 25-NOV-1993.  
 PD  
 XX



## RESULT 11

AAAD12894  
ID AAD12894 standard; DNA; 36 BP.  
XX AC AAD12894;  
XX DT 16-OCT-2001 (first entry)  
XX DE Bcl-2-IgH fusion gene comprising chromosomal translocation t(14;18).  
XX DE Human; double stranded RNA dependent protein kinase; PKR; genetic locus;  
XX KW antisense; therapy; proliferative disorder; neoplastic disease;  
XX KW psoriasis; vasculogenesis; angiogenesis; apoptosis; cytostatic; bcl-2;  
XX KW immunoglobulin heavy chain; IgH; fusion protein; DCLL;  
XX KW follicular lymphoma; FT; chromosomal translocation; ds.  
XX OS Homo sapiens.  
XX PN WO200157205-A1.  
XX FH Key Location/Qualifiers  
XX FT misc\_feature 20..21  
XX FT /\*tag= a  
XX FT /note= "Translocation occurring site"  
XX PN WO200157205-A1.  
XX PD 09-AUG-2001.  
XX PF 31-JAN-2001; 2001WO-IL00094.  
XX PR 31-JAN-2000; 2000US-0179361.  
XX PR 23-DEC-2000; 2000US-0258010.  
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
XX PI Shir A, Levitzky A;  
XX DR WPI; 2001-488878/53.  
XX PT Activating double stranded RNA dependent protein kinase in targeted  
XX PT cell population, by hybridizing antisense RNA with sequence at single  
XX PT genetic locus in the population, that is absent in non-targeted  
XX PT population  
XX PS Disclosure; Page 12; 54pp; English.  
XX CC The present invention relates to a method for selective killing of cells  
XX CC in a targeted cell population by selectively activating double stranded  
XX CC (ds) RNA dependent protein kinase (PKR). The method involves selecting  
XX CC sequence at single genetic locus in targeted cell population that is  
XX CC absent from equivalent locus in non-targeted cell population, obtaining  
XX CC anti-sense RNA having sequence homology with the genetic locus, and  
XX CC permitting anti-sense RNA to hybridise with the RNA transcribed from the  
XX CC genetic locus to form contiguous dsRNA for activating PKR. The method is  
XX CC also used for treating proliferative disorders such as neoplastic  
XX CC disease, psoriasis and vasculogenesis or angiogenesis. The present  
XX CC sequence is an antiapoptotic bcl-2-immunoglobulin heavy chain (IgH) locus  
XX CC fusion gene comprising chromosomal translocation t(14;18)(q32;q21). The  
XX CC DCLL and follicular lymphoma (FT) is characterised by the chromosomal  
XX CC translocation of bcl-2-IgH fusion gene.  
XX SQ Sequence 36 BP; 15 A; 4 C; 10 G; 7 T; 0 other;  
Query Match 0.6%; Score 32.8; DB 22; Length 36;  
Best Local Similarity 94.4%; Pred. No. 9.7e+02;  
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4098 CAAAGCATTCGTGAGAGGTGAGATAGCCCTGAGT 4133  
|||||  
DB 1 CAAAGCATTCGTGAGAGGTGAGATAGCACTGAGT 36

## RESULT 12

AAAD12893/c  
ID AAD12893 standard; RNA; 36 BP.  
XX AC AAD12893;  
XX DT 16-OCT-2001 (first entry)  
XX DE Anti-sense RNA targetted to bcl-2-IgH fusion gene.  
XX DE Human; double stranded RNA dependent protein kinase; PKR; genetic locus;  
XX KW antisense; therapy; proliferative disorder; neoplastic disease;  
XX KW psoriasis; vasculogenesis; angiogenesis; apoptosis; cytostatic; bcl-2;  
XX KW immunoglobulin heavy chain; IgH; fusion protein; DCLL;  
XX KW follicular lymphoma; FT; chromosomal translocation; ss.  
XX OS Homo sapiens.  
XX PN WO200157205-A1.  
XX PD 09-AUG-2001.  
XX PF 31-JAN-2001; 2001WO-IL00094.  
XX PR 31-JAN-2000; 2000US-0179361.  
XX PR 22-DEC-2000; 2000US-0258010.  
XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
XX PI Shir A, Levitzky A;  
XX DR WPI; 2001-488878/53.  
XX PT Activating double stranded RNA dependent protein kinase in targeted  
XX PT cell population, by hybridizing antisense RNA with sequence at single  
XX PT genetic locus in the population, that is absent in non-targeted  
XX PT population  
XX PS Claim 30; Page 12; 54pp; English.  
XX CC The present invention relates to a method for selective killing of cells  
XX CC in a targeted cell population by selectively activating double stranded  
XX CC (ds) RNA dependent protein kinase (PKR). The method involves selecting  
XX CC sequence at single genetic locus in targeted cell population that is  
XX CC absent from equivalent locus in non-targeted cell population, obtaining  
XX CC anti-sense RNA having sequence homology with the genetic locus, and  
XX CC permitting anti-sense RNA to hybridise with the RNA transcribed from the  
XX CC genetic locus to form contiguous dsRNA for activating PKR. The method is  
XX CC also used for treating proliferative disorders such as neoplastic  
XX CC disease, psoriasis and vasculogenesis or angiogenesis. The present  
XX CC sequence is an anti-sense RNA targetted to antiapoptotic  
XX CC bcl-2-immunoglobulin heavy chain (IgH) locus fusion gene. The DCLL and  
XX CC follicular lymphoma (FT) is characterised by a t(14;18)(q32;q21)  
XX CC chromosomal translocation of bcl-2-IgH fusion gene.  
XX SQ Sequence 36 BP; 7 A; 11 C; 3 G; 15 U; 0 other;  
Query Match 0.6%; Score 31.2; DB 22; Length 36;  
Best Local Similarity 91.7%; Pred. No. 2.2e+03;  
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4098 CAAAGCATTCGTGAGAGGTGAGATAGCCCTGAGT 4133  
|||||  
DB 36 CAAAGGATTCGTGAGAGGTGAGATAGCACTGAGT 1  
|||||  
RESULT 13  
AAAT35442  
ID AAT35442 standard; DNA; 30 BP.  
XX AC AAT35442;  
XX DT 27-MAY-1997 (first entry)

```

XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.
XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;
XX KW t14; t16; q21; q21; N region; antisense; expression; inhibitor;
XX KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;
XX KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX OS
XX PN WO9627663-A2.
XX PD
XX PD 12-SEP-1996.
XX PF 02-MAR-1996; 96WO-EP00852.
XX PF 03-MAR-1995; 95TT-OMI0420.
XX PF (CNDR ) CONSIGLIO NAZ DELLE RICERCHE.
XX PA Capaccioli S, Morelli S, Nicolin A;
XX PI WPI; 1996-425424/42.
XX DR
XX XX
XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)
XX PT translocated cells - used to develop oligodeoxynucleotides for the
XX PT diagnosis and treatment of tumours associated with the
XX PT translocation.
XX PS Example 1; Page 11; 32pp; English.
XX PS
XX CC AAT35441-T35443 are PCR primers used to amplify the chimeric bcl-2/IgH
XX CC (immunoglobulin heavy chain) gene present in the t(14; 18) chromosomally
XX CC translocated non-Hodgkin's lymphoma cell line DOHH-2. The transcript
XX CC produced is used for the design of antisense transcripts which can
XX CC inhibit the production of bcl-2 protein in t(14; 18) translocated cells
XX CC and induce cell death. The antisense transcripts can be used for the
XX CC diagnosis and treatment of t(14; 18)-associated tumours and for
XX CC monitoring treatment of a pathology associated with a t(14; 18)
XX CC translocation.
XX SQ Sequence 30 BP; 3 A; 9 C; 6 G; 12 T; 0 other;
XX
Query Match 0.6%; Score 30; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4256 GACCTGTGTTCTGGAAGGTTCTCTGTCCTCC 4285
DB 1 GACCTGTGTTCTGGAAGGTTCTCTGTCCTCC 30
RESULT 14
AAT66066
ID AAT66066 standard; DNA; 30 BP.
AC AAT66066;
XX
XX 18-JUN-1997 (first entry)
XX
XX (dC-dA)n.(dG-dT)n polymorphic repeat sequence #7.
XX
XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;
XX KW hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX
XX US5582979-A.
XX PN
XX 10-DEC-1996.
XX PD

```

```

XX 21-APR-1989; 89US-0341562.
XX
XX 05-SEP-1991; 91US-0754351.
XX PR 21-APR-1989; 89US-0341562.
XX PR 04-APR-1994; 94US-0222177.
XX
XX (MARS-) MARSHFIELD CLINIC.
XX
XX Weber JL;
XX
XX WPI; 1997-042299/04.
XX
XX Detection of polymorphic genetic markers of the form
XX (dC-dA)n(dG-dT)n - using novel nucleic acid moles. as primers
XX
XX Example 8; Column 57-58; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
XX having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
XX markers. Primers based on these sequences can be used to detect these
XX repeats, especially for use in e.g. paternity or maternity testing,
XX human genetic analysis such as linkage analysis of genetic disease,
XX commercial animal or plant breeding or pedigree analysis.
XX
XX The repeats, when analysed, fall into 4 categories:
XX 1) perfect repeats which are alternating tandem CA repeats with no
XX interruptions and without adjacent repeats of another sequence;
XX 2) imperfect repeats which are defined as 2 or more runs of uninterrupted
XX CA repeats separated by no more than 3 consecutive non-repeat bases;
XX 3) compound perfect repeats which are uninterrupted runs of CA separated
XX by no more than 3 consecutive non-repeat bases from a run of at least
XX 5 uninterrupted dinucleotide or longer repeats of a sequence other than
XX (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted mononucleotides; and
XX 4) imperfect compound repeats which are defined as for the perfect
XX compound repeats except that the runs of CA are interrupted.
XX This sequence is an example of an imperfect repeat sequence of structure:
XX (CA)5G(ACA)G(AC)7A.
XX
XX SQ Sequence 30 BP; 15 A; 13 C; 2 G; 0 U; 0 other;
XX
Query Match 0.6%; Score 30; DB 18; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2310 CACACACACACACACACACACACACACACA 2339
DB 1 CACACACACACACACACACACACACACACA 30
RESULT 15
AAQ68850
ID AAQ68850 standard; DNA; 38 BP.
XX
XX AAQ68850;
XX
XX 28-OCT-1994 (first entry)
XX
XX Human chromosomal repeat element.
XX
XX Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR;
XX KW sequence tagged site; genetic disorder; diagnosis; abnormality;
XX KW Prader-Willi; Angelman; Beckwith-Wiedemann; syndrome; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX repeat_region 5..38
XX /*tag= a
XX repeat_unit 5..6
XX /*tag= b
XX
XX WO9406936-A.

```





XX PI Capaccioli S, Morelli S, Nicolin A;  
 XX DR WPI; 1996-425424/42.  
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)  
 PT translocated cells - used to develop oligodeoxynucleotides for the  
 PT diagnosis and treatment of tumours associated with the  
 XX translocation.  
 XX PS Example 1; Page 12; 32pp; English.  
 XX CC AAT35441-T35443 are PCR primers used to amplify the chimeric bcl-2/IgH  
 CC (immunoglobulin heavy chain) gene present in the t(14; 18) chromosomally  
 CC translocated non-Hodgkin's lymphoma cell line DOHH-2. The transcript  
 CC produced is used for the design of antisense transcripts which can  
 CC inhibit the production of bcl-2 protein in t(14; 18) translocated cells  
 CC and induce cell death. The antisense transcripts can be used for the  
 CC diagnosis and treatment of t(14; 18)-associated tumours and for  
 CC monitoring treatment of a pathology associated with a t(14; 18)  
 CC translocation.  
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;  
 XX  
 XX Query Match 0.6%; Score 28; DB 17; Length 30;  
 XX Best Local Similarity 100.0%; Pred. No. 1e+04;  
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 4504 CTTGAGGCTCTCTGAAATGCAGTGGT 4531  
 Db 30 CTTGAGGCTCTCTGAAATGCAGTGGT 3  
 RESULT 18  
 AAT35446/C  
 ID AAT35446 standard; DNA; 30 BP.  
 XX AC AAT35446;  
 XX DT 27-MAY-1997 (first entry)  
 XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.  
 XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;  
 KW t14; t18; q32; q21; N region; antisense; expression; inhibitor;  
 KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;  
 KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;  
 KW polymerase chain reaction; ss.  
 XX Synthetic.  
 XX WO9627663-A2.  
 XX PD 12-SEP-1996.  
 XX PF 02-MAR-1996; 96WO-EP00852.  
 XX PR 03-MAR-1995; 95IT-OMI0420.  
 XX PA (CNR ) CONSIGLIO NAZ DELLE RICERCHE.  
 XX PI Capaccioli S, Morelli S, Nicolin A;  
 XX DR WPI; 1996-425424/42.  
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)  
 PT translocated cells - used to develop oligodeoxynucleotides for the  
 PT diagnosis and treatment of tumours associated with the  
 XX translocation.  
 XX PS Example 1; Page 12; 32pp; English.  
 XX CC AAT35446 and AAT35447 are PCR primers used to amplify the chimeric  
 CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)  
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The  
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The  
 CC transcript produced is used for the design of antisense transcripts  
 CC which can inhibit the production of bcl-2 protein in t(14; 18)  
 CC translocated cells and induce cell death. The antisense transcripts can  
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours  
 CC and for monitoring treatment of a pathology associated with a t(14; 18)  
 CC translocation.  
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;  
 XX  
 XX Query Match 0.6%; Score 28; DB 17; Length 30;  
 XX Best Local Similarity 100.0%; Pred. No. 1e+04;  
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 4504 CTTGAGGCTCTCTGAAATGCAGTGGT 4531  
 Db 30 CTTGAGGCTCTCTGAAATGCAGTGGT 3  
 RESULT 18  
 AAT35446/C  
 ID AAT35446 standard; DNA; 30 BP.  
 XX AC AAT35446;  
 XX DT 27-MAY-1997 (first entry)  
 XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.  
 XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;  
 KW t14; t18; q32; q21; N region; antisense; expression; inhibitor;  
 KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;  
 KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;  
 KW polymerase chain reaction; ss.  
 XX Synthetic.  
 XX WO9627663-A2.  
 XX PD 12-SEP-1996.  
 XX PF 02-MAR-1996; 96WO-EP00852.  
 XX PR 03-MAR-1995; 95IT-OMI0420.  
 XX PA (CNR ) CONSIGLIO NAZ DELLE RICERCHE.  
 XX PI Capaccioli S, Morelli S, Nicolin A;  
 XX DR WPI; 1996-425424/42.  
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)  
 PT translocated cells - used to develop oligodeoxynucleotides for the  
 PT diagnosis and treatment of tumours associated with the  
 XX translocation.  
 XX PS Example 1; Page 12; 32pp; English.  
 XX CC AAT35446 and AAT35447 are PCR primers used to amplify the chimeric

CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)  
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The  
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The  
 CC transcript produced is used for the design of antisense transcripts  
 CC which can inhibit the production of bcl-2 protein in t(14; 18)  
 CC translocated cells and induce cell death. The antisense transcripts can  
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours  
 CC and for monitoring treatment of a pathology associated with a t(14; 18)  
 CC translocation.  
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;  
 XX  
 XX Query Match 0.6%; Score 28; DB 17; Length 30;  
 XX Best Local Similarity 100.0%; Pred. No. 1e+04;  
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 4504 CTTGAGGCTCTCTGAAATGCAGTGGT 4531  
 Db 30 CTTGAGGCTCTCTGAAATGCAGTGGT 3  
 RESULT 19  
 AAT35447/C  
 ID AAT35447 standard; DNA; 30 BP.  
 XX AC AAT35447;  
 XX DT 27-MAY-1997 (first entry)  
 XX DE Non-Hodgkin's B cell line bcl-2/IgH chimeric gene PCR primer.  
 XX KW Non-Hodgkin's lymphoma; cell line DOHH2; DHL-4; leukaemia; chromosome;  
 KW t14; t18; q32; q21; N region; antisense; expression; inhibitor;  
 KW bcl-2; IgH; immunoglobulin heavy chain; hybrid; cell death; tumour;  
 KW cancer; neoplasia; diagnosis; translocation; chimera; PCR;  
 KW polymerase chain reaction; ss.  
 XX Synthetic.  
 XX WO9627663-A2.  
 XX PD 12-SEP-1996.  
 XX PF 02-MAR-1996; 96WO-EP00852.  
 XX PR 03-MAR-1995; 95IT-OMI0420.  
 XX PA (CNR ) CONSIGLIO NAZ DELLE RICERCHE.  
 XX PI Capaccioli S, Morelli S, Nicolin A;  
 XX DR WPI; 1996-425424/42.  
 XX PT New chimeric bcl-2/IgH antisense transcript of t(14; 18)  
 PT translocated cells - used to develop oligodeoxynucleotides for the  
 PT diagnosis and treatment of tumours associated with the  
 XX translocation.  
 XX PS Example 1; Page 12; 32pp; English.  
 XX CC AAT35446 and AAT35447 are PCR primers used to amplify the chimeric  
 CC bcl-2/IgH (immunoglobulin heavy chain) gene present in the t(14; 18)  
 CC chromosomally translocated non-Hodgkin's lymphoma cell line DOHH-2. The  
 CC primers correspond to the 3' untranslated region of the bcl-2 gene. The  
 CC transcript produced is used for the design of antisense transcripts  
 CC which can inhibit the production of bcl-2 protein in t(14; 18)  
 CC translocated cells and induce cell death. The antisense transcripts can  
 CC be used for the diagnosis and treatment of t(14; 18)-associated tumours  
 CC and for monitoring treatment of a pathology associated with a t(14; 18)  
 CC translocation.  
 XX Sequence 30 BP; 9 A; 9 C; 7 G; 5 T; 0 other;  
 XX









XX SQ Sequence 27 BP; 6 A; 7 G; 7 C; 7 T; 0 other;  
 Query Match 0.5%; Score 27; DB 24; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1970 ACAACATCGCCCTGTGGATGACTGAGT 1996  
 |||||  
 Db 27 ACAACATCGCCCTGTGGATGACTGAGT 1

RESULT 30  
 AAQ33737/c  
 ID AAQ33737 standard; DNA; 39 BP.  
 XX  
 AC AC AC  
 XX  
 XX  
 02-FEB-1993 (first entry)  
 XX  
 DE Microsatellite sequence from clone TGLA153.  
 XX  
 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 KW  
 OS Bos taurus.  
 XX  
 XX WO9213102-A.  
 PN  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92WO-US00340.  
 XX  
 XX 15-JAN-1991; 91US-0642342.  
 PR  
 XX  
 XX (GENM-) GENMARK.  
 PA  
 XX  
 XX Georges M, Massey JM;  
 PI  
 XX  
 XX WPI; 1992-284684/34.  
 DR  
 XX  
 PT Polymorphic bovine DNA markers - used in genetic identification,  
 PT gene mapping, and selective breeding  
 XX  
 XX Table 7; Page 225; 517pp; English.  
 XX  
 CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between  
 CC 250 and 500 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe.  
 CC One out of 50 clones cross-hybridised. Assuming independent  
 CC distribution of microsatellites and MboI sites, the frequency of  
 CC (T6)n > 9 microsatellites in the bovine genome is estimated at >100,  
 CC 000. The sequence information for ca. 230 such bovine microsatellites  
 CC is summarised in the specification and indexed herein (see below).  
 CC The sequences upstream and downstream of the microsatellite sequence  
 CC were used to generate the required PCR primers for in vitro  
 CC amplification of the corresp. microsatellite (using the program  
 CC OPTIPRIM). The microsatellites may be used to identify individuals,  
 CC for parentage testing, and in the genetic mapping of economic trait  
 CC loci, or genes involved in the determination of economically important  
 CC traits esp. in cattle, to allow selective breeding.  
 CC See also AAQ33501-34437.  
 XX  
 XX Sequence 39 BP; 2 A; 0 C; 17 G; 20 T; 0 other;  
 XX

Query Match 0.5%; Score 27; DB 13; Length 39;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+04;  
 Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACAGACACACACACACACACAAT 2344  
 |||||  
 Db 38 CACACACACACACACACACACACACACACAT 4







BEST LOCAL SIMILARITY 55.5%, AREA: 100%

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MbOI DNA fragments of between 250 and 500 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MbOI sites, the frequency of (T<sub>6</sub>)<sub>n</sub> >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for *in vivo*





The invention relates to the isolation of polymorphic repeat sequences having the sequence (dG-dA)<sub>n</sub> (dG-dT)<sub>n</sub> which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g. paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones

The present invention describes an isolated nucleotide sequence (I) encoding at least a portion of the human alpha-7 neuronal nicotinic acetylcholine receptor (alpha7-hnAChR). Also described are: (1) a peptide encoded by (1); (2) a vector comprising (1); (3) a host cell transformed with a vector of (2); (4) a polynucleotide comprising at least 15 nucleotides which hybridises under stringent conditions to at least a portion of (1); (5) a method for detection of a polynucleotide encoding alpha 7-hnAChR in a biological sample; and (6) a method for amplification of nucleic acid from a sample suspected of containing nucleic acid encoding alpha 7-hnAChR. The primers and probes from the present invention can be used on brain tissue and blood samples of humans suspected of suffering from schizophrenia, small cell lung carcinoma, breast cancer and nicotine-dependent illness. This is particularly useful for diagnosis of schizophrenia. Other illnesses that can be studied/diagnosed are epilepsy (e.g. juvenile myoclonic

ID	ABK24296 standard; DNA; 32 BP.
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

1000

Matches	28;	Conservative	0;	Mismatches	2;	Indels
---------	-----	--------------	----	------------	----	--------



```

XX PN US582979-A.
XX PD 10-DEC-1996.
XX PF 21-APR-1989; 89US-0341562.
XX PR 05-SEP-1991; 91US-0754351.
XX PR 21-APR-1989; 89US-0341562.
XX PR 04-APR-1994; 94US-0222177.
XX PA (MARS-) MARSHFIELD CLINIC.
XX PI Weber JL;
XX DR WPI; 1997-042299/04.
XX PT Detection of polymorphic genetic markers of the form
XX PS (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX PS Claim 1; Column 9-10; 186pp; English.
XX CC The invention relates to the isolation of polymorphic repeat sequences
XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
XX CC markers. Primers based on these sequences can be used to detect these
XX CC repeats, especially for use in e.g. paternity or maternity testing,
XX CC human genetic analysis such as linkage analysis of genetic disease,
XX CC commercial animal or plant breeding or pedigree analysis. Clones
XX CC containing the repeat sequences were isolated by hybridisation of
XX CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
XX CC probe. Over 100 repeat blocks were isolated. The inserts from the
XX CC clones were amplified by primers AAT65798-T66047. Those clones where the
XX CC repeat sequence has been determined are shown in AAT65704-797. This
XX CC repeat sequence is from the marker clone Mdf3 which contains the repeat
XX CC sequence having the formula: (CA)16C.
XX SQ Sequence 33 BP; 16 A; 17 C; 0 G; 0 U; 0 other;
XX
Query Match 0.5%; Score 26.8; DB 18; Length 33;
Best Local Similarity 93.3%; Pred. No. 1.9e+04;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2310 CACACACACAGACACACACACACACACA 2339
DB 1 CACACACACACACACACACACACACACA 30
|||||
RESULT 50
AAT65754
ID AAT65754 standard; DNA; 33 BP.
XX AC AAT65754;
XX DT 17-JUN-1997 (first entry)
XX DE Repeat sequence from polymorphic marker clone Mfd58.
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;
XX KW hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX PN US582979-A.
XX PD 10-DEC-1996.
XX PF 21-APR-1989; 89US-0341562.
XX PR 05-SEP-1991; 91US-0754351.
XX PR 21-APR-1989; 89US-0341562.
XX PR 04-APR-1994; 94US-0222177.

```

```

XX PA (MARS-) MARSHFIELD CLINIC.
XX PI Weber JL;
XX DR WPI; 1997-042299/04.
XX PT Detection of polymorphic genetic markers of the form
XX PS (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
XX PS Disclosure; Column 11-12; 186pp; English.
XX CC The invention relates to the isolation of polymorphic repeat sequences
XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
XX CC markers. Primers based on these sequences can be used to detect these
XX CC repeats, especially for use in e.g. paternity or maternity testing,
XX CC human genetic analysis such as linkage analysis of genetic disease,
XX CC commercial animal or plant breeding or pedigree analysis. Clones
XX CC containing the repeat sequences were isolated by hybridisation of
XX CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
XX CC probe. Over 100 repeat blocks were isolated. The inserts from the
XX CC clones were amplified by primers AAT65798-T66047. Those clones where the
XX CC repeat sequence has been determined are shown in AAT65704-797. This
XX CC repeat sequence is from the marker clone Mdf58 which contains the repeat
XX CC sequence having the formula: (CA)16.5.
XX SQ Sequence 33 BP; 16 A; 17 C; 0 G; 0 U; 0 other;
XX
Query Match 0.5%; Score 26.8; DB 18; Length 33;
Best Local Similarity 93.3%; Pred. No. 1.9e+04;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2310 CACACACACAGACACACACACACACACA 2339
DB 1 CACACACACACACACACACACACACACA 30
|||||
Search completed: May 31, 2003, 16:59:59
Job time : 1020 secs

```





GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 16:41:01 ; Search time 610 Seconds  
(without alignments)  
11242.271 Million cells

Title: US-09-375-514-19  
Perfect score: 5086  
Sequence: 1 acagccagccccctccg

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues  
Total number of hits satisfying chosen parameters: 471460

Minimum DB seq	length: 10
Maximum DB seq	length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

```

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Query		Length	DB	ID	Description
		Match					
C 1	26.8	0.5	31	9	US-10-085-906-27		Sequence 27, Appl
C 2	26.8	0.5	39	10	US-09-263-959-678		Sequence 678, App
C 3	25.8	0.5	30	9	US-10-085-906-93		Sequence 93, Appl
C 4	25.2	0.5	34	10	US-09-263-959-711		Sequence 711, App
C 5	24.2	0.5	29	10	US-09-263-959-665		Sequence 665, App
C 6	24	0.5	24	10	US-09-920-342-9		Sequence 9, Appl
7	24	0.5	24	10	US-09-920-342-11		Sequence 11, Appl
C 8	23.8	0.5	27	10	US-09-735-363A-1		Sequence 1, Appl
C 9	23.8	0.5	27	10	US-09-735-363A-5		Sequence 5, Appl
C 10	23.8	0.5	27	10	US-09-735-363A-66		Sequence 66, Appl
C 11	23.8	0.5	27	10	US-09-263-959-770		Sequence 770, App
C 12	23.6	0.5	30	10	US-09-263-959-600		Sequence 600, App
C 13	22.4	0.4	24	9	US-09-970-820-11		Sequence 11, Appl
C 14	22.4	0.4	24	9	US-09-986-718-11		Sequence 11, Appl
C 15	22.4	0.4	24	10	US-09-371-900-11		Sequence 11, Appl
16	22	0.4	22	9	US-09-931-732-21		Sequence 21, Appl
17	21.4	0.4	33	10	US-09-925-674A-1		Sequence 1, Appl
18	21.2	0.4	31	9	US-10-231-381-27		Sequence 27, Appl
C 19	21	0.4	31	10	US-09-925-674A-3		Sequence 3, Appl

c 93	18	0.4	18	9	US-09-835-370-21	Sequence 21, Appl	166	17.6	0.3	24	9	US-10-035-958-19	Sequence 19, Appl
c 94	18	0.4	18	9	US-09-888-326-755	Sequence 755, Appl	167	17.6	0.3	24	9	US-10-036-150-19	Sequence 19, Appl
c 95	18	0.4	18	9	US-09-888-326-756	Sequence 756, Appl	168	17.6	0.3	24	9	US-10-036-150-19	Sequence 19, Appl
c 96	18	0.4	18	9	US-09-931-732-20	Sequence 20, Appl	169	17.6	0.3	24	12	US-10-036-342-19	Sequence 19, Appl
c 97	18	0.4	18	9	US-09-818-918-55	Sequence 55, Appl	170	17.6	0.3	25	9	US-10-060-830-506	Sequence 506, Appl
c 98	18	0.4	18	9	US-10-112-653-1	Sequence 1, Appl	171	17.6	0.3	25	9	US-10-060-830-506	Sequence 506, Appl
c 99	18	0.4	18	9	US-10-112-653-85	Sequence 85, Appl	c 172	17.6	0.3	25	10	US-09-866-108-3882	Sequence 3882, Ap
c 100	18	0.4	18	9	US-10-017-995-1	Sequence 1, Appl	c 173	17.6	0.3	25	10	US-09-866-108-3882	Sequence 3882, Ap
c 101	18	0.4	18	9	US-10-017-995-54	Sequence 54, Appl	c 174	17.6	0.3	30	10	US-09-725-720-25	Sequence 25, Appl
c 102	18	0.4	18	9	US-10-017-995-55	Sequence 55, Appl	175	17.6	0.3	31	10	US-09-801-274-399	Sequence 399, App
c 103	18	0.4	18	9	US-10-017-995-91	Sequence 91, Appl	176	17.6	0.3	33	10	US-09-263-959-825	Sequence 825, App
c 104	18	0.4	18	9	US-09-776-479-1	Sequence 1, Appl	177	17.6	0.3	34	9	US-09-769-787-383	Sequence 383, App
c 105	18	0.4	18	9	US-09-776-479-54	Sequence 54, Appl	178	17.6	0.3	35	9	US-10-012-896-815	Sequence 815, App
c 106	18	0.4	18	9	US-09-776-479-55	Sequence 55, Appl	179	17.6	0.3	35	9	US-09-895-793-815	Sequence 815, App
c 107	18	0.4	18	9	US-09-776-479-91	Sequence 91, Appl	180	17.6	0.3	35	9	US-09-895-814-815	Sequence 815, App
c 108	18	0.4	18	9	US-10-002-884A-6	Sequence 6, Appl	181	17.6	0.3	35	10	US-09-426-548-34	Sequence 34, Appl
c 109	18	0.4	18	9	US-10-300-247-51	Sequence 51, Appl	182	17.6	0.3	35	10	US-09-759-143-815	Sequence 815, App
c 110	18	0.4	18	10	US-09-824-468-59	Sequence 59, Appl	183	17.6	0.3	35	10	US-09-780-669-815	Sequence 815, App
c 111	18	0.4	18	10	US-09-824-468-104	Sequence 104, Appl	184	17.6	0.3	35	10	US-09-822-827-815	Sequence 815, App
c 112	18	0.4	18	10	US-09-965-116A-7	Sequence 7, Appl	c 185	17.6	0.3	38	9	US-09-780-533A-4212	Sequence 4212, Ap
c 113	18	0.4	18	10	US-09-965-116A-77	Sequence 77, Appl	c 186	17.6	0.3	39	9	US-10-080-980-24	Sequence 24, Appl
c 114	18	0.4	18	10	US-09-965-116A-98	Sequence 98, Appl	c 187	17.6	0.3	39	9	US-10-104-943-38	Sequence 38, Appl
c 115	18	0.4	18	10	US-09-965-116A-99	Sequence 99, Appl	c 188	17.6	0.3	39	9	US-10-104-943-82	Sequence 82, Appl
c 116	18	0.4	18	9	US-09-974-974-13	Sequence 13, Appl	c 189	17.6	0.3	39	9	US-10-104-943-84	Sequence 84, Appl
c 117	18	0.4	18	9	US-09-888-326-757	Sequence 757, Appl	c 190	17.6	0.3	39	9	US-10-104-943-88	Sequence 88, Appl
c 118	18	0.4	18	9	US-10-112-653-81	Sequence 81, Appl	c 191	17.6	0.3	39	9	US-10-104-943-90	Sequence 90, Appl
c 119	18	0.4	18	9	US-10-017-995-87	Sequence 87, Appl	c 192	17.6	0.3	40	9	US-10-222-952A-6	Sequence 6, Appl
c 120	18	0.4	18	9	US-09-982-262B-59	Sequence 59, Appl	c 193	17.6	0.3	40	10	US-09-790-417-215	Sequence 215, App
c 121	18	0.4	18	9	US-09-776-479-87	Sequence 87, Appl	c 194	17.6	0.3	40	10	US-09-245-802-4	Sequence 4, Appl
c 122	18	0.4	18	9	US-09-754-853A-601	Sequence 601, Appl	c 195	17.4	0.3	19	10	US-09-557-423-7	Sequence 7, Appl
c 123	18	0.4	18	27	US-10-066-151-92	Sequence 92, Appl	c 196	17.4	0.3	19	10	US-09-557-423-8	Sequence 8, Appl
c 124	18	0.4	18	29	US-09-817-387-12	Sequence 12, Appl	c 197	17.4	0.3	19	10	US-09-932-129-7	Sequence 7, Appl
c 125	18	0.4	18	32	US-10-183-695-1	Sequence 1, Appl	c 198	17.4	0.3	19	10	US-09-969-373-3086	Sequence 3086, Ap
c 126	18	0.4	18	34	US-10-085-906-126	Sequence 126, Appl	c 199	17.4	0.3	20	9	US-10-085-906-33	Sequence 33, Appl
c 127	18	0.4	18	34	US-10-134-021-12	Sequence 12, Appl	c 200	17.4	0.3	20	9	US-10-165-854-1	Sequence 1, Appl
c 128	18	0.4	18	34	US-09-810-796-16	Sequence 16, Appl	c 201	17.4	0.3	20	9	US-10-165-854-2	Sequence 2, Appl
c 129	18	0.4	18	36	US-09-828-034-5	Sequence 5, Appl	c 202	17.4	0.3	27	9	US-10-085-906-123	Sequence 123, App
c 130	18	0.4	18	39	US-10-288-357-4	Sequence 4, Appl	c 203	17.4	0.3	30	9	US-09-968-033C-9	Sequence 9, Appl
c 131	18	0.4	18	39	US-10-066-151-62	Sequence 62, Appl	c 204	17.4	0.3	30	9	US-09-984-842-2	Sequence 2, Appl
c 132	18	0.4	18	40	US-09-245-802-70	Sequence 70, Appl	c 205	17.4	0.3	30	10	US-09-932-129-9	Sequence 9, Appl
c 133	18	0.4	18	40	US-09-993-170-17	Sequence 17, Appl	c 206	17.4	0.3	31	9	US-10-194-138-1	Sequence 1, Appl
c 134	17.8	0.3	21	9	US-10-112-653-876	Sequence 876, Appl	c 207	17.4	0.3	31	10	US-09-801-274-450	Sequence 450, App
c 135	17.8	0.3	21	9	US-10-017-995-907	Sequence 907, Appl	c 208	17.4	0.3	31	10	US-09-801-274-1391	Sequence 1391, Ap
c 136	17.8	0.3	21	9	US-10-085-906-412	Sequence 412, Appl	c 209	17.4	0.3	33	9	US-10-021-330-1	Sequence 1, Appl
c 137	17.8	0.3	21	9	US-09-776-479-907	Sequence 907, Appl	c 210	17.4	0.3	33	9	US-09-852-416-23	Sequence 23, Appl
c 138	17.8	0.3	21	10	US-09-735-363A-19	Sequence 19, Appl	c 211	17.4	0.3	33	10	US-09-859-854-23	Sequence 23, Appl
c 139	17.8	0.3	21	10	US-09-735-363A-20	Sequence 20, Appl	c 212	17.4	0.3	34	9	US-10-114-893-256	Sequence 256, App
c 140	17.8	0.3	21	10	US-09-828-034-10	Sequence 10, Appl	c 213	17.4	0.3	34	9	US-10-124-880-54	Sequence 54, Appl
c 141	17.8	0.3	29	10	US-09-996-606-4	Sequence 4, Appl	c 214	17.4	0.3	34	10	US-09-765-272-380	Sequence 380, App
c 142	17.8	0.3	30	9	US-10-042-193A-1	Sequence 1, Appl	c 215	17.4	0.3	35	9	US-10-095-672A-20	Sequence 20, Appl
c 143	17.8	0.3	30	9	US-10-042-193A-2	Sequence 2, Appl	c 216	17.4	0.3	35	10	US-09-804-615-25	Sequence 25, Appl
c 144	17.8	0.3	30	9	US-10-217-914-4	Sequence 4, Appl	c 217	17.4	0.3	36	9	US-09-957-995A-24	Sequence 24, Appl
c 145	17.8	0.3	30	9	US-10-057-467-12	Sequence 12, Appl	c 218	17.4	0.3	36	9	US-09-961-404-14	Sequence 14, Appl
c 146	17.8	0.3	31	10	US-09-801-274-262	Sequence 262, Appl	c 219	17.4	0.3	36	10	US-09-828-034-4	Sequence 4, Appl
c 147	17.8	0.3	31	10	US-09-801-274-438	Sequence 438, Appl	c 220	17.4	0.3	36	10	US-09-932-129-10	Sequence 10, Appl
c 148	17.8	0.3	32	9	US-10-260-923-1	Sequence 1, Appl	c 221	17.4	0.3	36	10	US-09-870-203A-29	Sequence 29, Appl
c 149	17.8	0.3	32	10	US-09-456-038-1	Sequence 1, Appl	c 222	17.4	0.3	36	10	US-09-870-203A-30	Sequence 30, Appl
c 150	17.8	0.3	34	10	US-09-263-959-803	Sequence 803, Appl	c 223	17.4	0.3	37	9	US-10-085-906-225	Sequence 225, App
c 151	17.8	0.3	38	9	US-10-085-906-285	Sequence 285, Appl	c 224	17.4	0.3	37	9	US-10-194-550-15	Sequence 15, Appl
c 152	17.8	0.3	38	9	US-09-500-700-51	Sequence 51, Appl	c 225	17.4	0.3	37	10	US-09-758-317-1	Sequence 1, Appl
c 153	17.8	0.3	38	9	US-09-848-754A-5701	Sequence 5701, Ap	c 226	17.4	0.3	37	10	US-09-894-991-6	Sequence 6, Appl
c 154	17.8	0.3	39	9	US-09-934-060A-16	Sequence 16, Appl	c 227	17.4	0.3	38	9	US-10-208-357-2	Sequence 2, Appl
c 155	17.8	0.3	39	10	US-09-774-414-20	Sequence 20, Appl	c 228	17.4	0.3	38	9	US-09-780-164-1733	Sequence 1733, Ap
c 156	17.8	0.3	40	9	US-10-135-965-8	Sequence 8, Appl	c 229	17.4	0.3	38	10	US-09-774-414-27	Sequence 27, Appl
c 157	17.8	0.3	40	9	US-10-135-965-37	Sequence 37, Appl	c 230	17.4	0.3	39	9	US-09-992-238-72	Sequence 72, Appl
c 158	17.8	0.3	40	9	US-10-135-965-51	Sequence 51, Appl	c 231	17.4	0.3	39	9	US-10-100-957A-147	Sequence 147, App
c 159	17.6	0.3	24	9	US-10-036-041-19	Sequence 19, Appl	c 232	17.4	0.3	39	9	US-10-120-604-93	Sequence 93, Appl
c 160	17.6	0.3	24	9	US-10-035-855-19	Sequence 19, Appl	c 233	17.4	0.3	39	9	US-10-120-604-97	Sequence 97, Appl
c 161	17.6	0.3	24	9	US-09-931-836-19	Sequence 19, Appl	c 234	17.4	0.3	40	10	US-09-823-257A-18	Sequence 18, Appl
c 162	17.6	0.3	24	9	US-10-036-214-19	Sequence 19, Appl	c 235	17.4	0.3	40	10	US-09-834-291-18	Sequence 18, Appl
c 163	17.6	0.3	24	9	US-10-035-719-19	Sequence 19, Appl	c 236	17.4	0.3	40	10	US-09-834-291-26	Sequence 26, Appl
c 164	17.6	0.3	24	9	US-10-036-160-19	Sequence 19, Appl	c 237	17.4	0.3	40	10	US-09-923-246-25	Sequence 25, Appl
c 165	17.6	0.3	24	9	US-09-974-546-71	Sequence 71, Appl	c 238	17.2	0.3	23	10	US-09-745-008-9	Sequence 9, Appl

us-09-375-514-19.rnpb

Sun Jun '1 14:55:56 2003

239	17.2	0.3	25	9	US-09-992-665-191	Sequence 191, Appl	c 312	17	0.3	36	10	US-09-306-417-16	Sequence 16, Appl
c 240	17.2	0.3	25	10	US-09-866-108-3880	Sequence 3880, Ap	c 313	17	0.3	37	9	US-09-908-504A-37	Sequence 37, Appl
c 241	17.2	0.3	25	10	US-09-866-108-3881	Sequence 3881, Ap	c 314	17	0.3	37	9	US-09-848-754A-6225	Sequence 6225, Ap
c 242	17.2	0.3	25	10	US-09-953-052-37	Sequence 37, Appl	c 315	17	0.3	38	9	US-09-780-164-1624	Sequence 1624, Ap
c 243	17.2	0.3	30	9	US-09-953-052-37	Sequence 17, Appl	c 316	17	0.3	38	9	US-09-930-423-1868	Sequence 1868, Ap
c 244	17.2	0.3	30	9	US-10-127-427-17	Sequence 22, Appl	c 317	17	0.3	38	9	US-09-930-423-2017	Sequence 2017, Ap
c 245	17.2	0.3	30	9	US-10-127-427-22	Sequence 17, Appl	c 318	17	0.3	38	9	US-10-067-956-40	Sequence 40, Appl
c 246	17.2	0.3	30	10	US-09-333-527-17	Sequence 22, Appl	c 319	17	0.3	39	9	US-10-080-980-24	Sequence 24, Appl
c 247	17.2	0.3	30	10	US-09-333-527-11	Sequence 11, Appl	c 320	17	0.3	39	9	US-09-853-745-34	Sequence 34, Appl
c 248	17.2	0.3	30	10	US-09-796-088-11	Sequence 11, Appl	c 321	17	0.3	39	10	US-09-903-452-22	Sequence 22, Appl
c 249	17.2	0.3	30	10	US-09-796-088-11	Sequence 11, Appl	c 322	17	0.3	39	10	US-09-540-991-3	Sequence 3, Appl
c 250	17.2	0.3	30	10	US-09-788-345-9	Sequence 9, Appl	c 323	17	0.3	39	10	US-09-774-414-20	Sequence 20, Appl
c 251	17.2	0.3	31	9	US-09-999-220B-28	Sequence 28, Appl	c 324	17	0.3	40	10	US-09-803-454-38	Sequence 38, Appl
c 252	17.2	0.3	31	9	US-09-999-220B-85	Sequence 85, Appl	c 325	17	0.3	40	10	US-09-915-060-48	Sequence 48, Appl
c 253	17.2	0.3	31	9	US-09-999-220B-97	Sequence 97, Appl	c 326	16.8	0.3	20	9	US-09-870-002-20	Sequence 20, Appl
c 254	17.2	0.3	31	9	US-09-848-754A-7504	Sequence 7504, Ap	c 327	16.8	0.3	20	9	US-09-888-326-410	Sequence 235, App
c 255	17.2	0.3	31	9	US-09-741-744A-110	Sequence 110, Appl	c 328	16.8	0.3	20	9	US-10-112-653-235	Sequence 243, App
c 256	17.2	0.3	34	9	US-09-778-900A-24	Sequence 24, Appl	c 329	16.8	0.3	20	9	US-10-017-995-243	Sequence 243, App
c 257	17.2	0.3	36	9	US-09-944-413-10	Sequence 10, Appl	c 330	16.8	0.3	20	9	US-09-776-479-243	Sequence 34, Appl
c 258	17.2	0.3	36	9	US-09-944-403-10	Sequence 10, Appl	c 331	16.8	0.3	20	10	US-09-734-846-34	Sequence 34, Appl
c 259	17.2	0.3	36	9	US-09-944-896-10	Sequence 10, Appl	c 332	16.8	0.3	20	10	US-09-734-846-46	Sequence 46, Appl
c 260	17.2	0.3	36	9	US-09-944-907-10	Sequence 10, Appl	c 333	16.8	0.3	20	10	US-09-734-847A-45	Sequence 45, Appl
c 261	17.2	0.3	36	9	US-09-944-929-10	Sequence 10, Appl	c 334	16.8	0.3	20	10	US-09-734-847A-48	Sequence 48, Appl
c 262	17.2	0.3	36	9	US-10-085-906-90	Sequence 90, Appl	c 335	16.8	0.3	20	10	US-09-734-847A-65	Sequence 65, Appl
c 263	17.2	0.3	36	9	US-09-944-884-10	Sequence 13, Appl	c 336	16.8	0.3	25	10	US-09-866-108-3878	Sequence 3878, Ap
c 264	17.2	0.3	36	9	US-09-968-255-13	Sequence 13, Appl	c 337	16.8	0.3	25	10	US-09-866-108-3879	Sequence 3879, Ap
c 265	17.2	0.3	36	9	US-09-944-852-10	Sequence 10, Appl	c 338	16.8	0.3	25	10	US-09-852-599-88	Sequence 88, Appl
c 266	17.2	0.3	36	9	US-09-943-780-10	Sequence 10, Appl	c 339	16.8	0.3	29	9	US-10-180-819-10	Sequence 10, Appl
c 267	17.2	0.3	36	10	US-09-866-028-10	Sequence 10, Appl	c 340	16.8	0.3	29	9	US-09-282-734-3	Sequence 3, Appl
c 268	17.2	0.3	36	10	US-09-944-449-10	Sequence 10, Appl	c 341	16.8	0.3	29	9	US-09-876-235-8	Sequence 26, Appl
c 269	17.2	0.3	36	10	US-09-944-457-10	Sequence 10, Appl	c 342	16.8	0.3	29	9	US-10-228-264-26	Sequence 27, Appl
c 270	17.2	0.3	36	10	US-09-973-322-15	Sequence 15, Appl	c 343	16.8	0.3	29	9	US-10-228-264-27	Sequence 28, Appl
c 271	17.2	0.3	36	10	US-09-945-587-10	Sequence 10, Appl	c 344	16.8	0.3	29	9	US-10-228-264-28	Sequence 29, Appl
c 272	17.2	0.3	36	10	US-09-945-015-10	Sequence 10, Appl	c 345	16.8	0.3	29	9	US-10-228-264-29	Sequence 37, Appl
c 273	17.2	0.3	36	10	US-09-944-396-10	Sequence 10, Appl	c 346	16.8	0.3	30	9	US-09-853-745-37	Sequence 13, Appl
c 274	17.2	0.3	36	10	US-09-944-432-10	Sequence 10, Appl	c 347	16.8	0.3	30	9	US-10-057-467-13	Sequence 34, Appl
c 275	17.2	0.3	36	10	US-09-944-654-10	Sequence 10, Appl	c 348	16.8	0.3	30	9	US-10-057-467-13	Sequence 7, Appl
c 276	17.2	0.3	36	10	US-09-943-851A-10	Sequence 10, Appl	c 349	16.8	0.3	30	9	US-10-263-766-7	Sequence 8, Appl
c 277	17.2	0.3	38	9	US-09-825-805-1249	Sequence 1249, Ap	c 350	16.8	0.3	30	10	US-10-209-608-8	Sequence 7, Appl
c 278	17.2	0.3	38	9	US-09-730-289B-1993	Sequence 1993, Ap	c 351	16.8	0.3	30	10	US-09-272-162-7	Sequence 7, Appl
c 279	17.2	0.3	38	10	US-09-765-272-354	Sequence 354, Appl	c 352	16.8	0.3	31	9	US-09-891-517-8	Sequence 3, Appl
c 280	17.2	0.3	39	9	US-09-309-196-109	Sequence 109, Appl	c 353	16.8	0.3	31	9	US-09-912-263-34	Sequence 34, Appl
c 281	17.2	0.3	39	9	US-09-846-430A-4	Sequence 4, Appl	c 354	16.8	0.3	31	9	US-09-912-263-37	Sequence 37, Appl
c 282	17.2	0.3	39	9	US-09-953-354-45	Sequence 45, Appl	c 355	16.8	0.3	31	10	US-09-801-274-111	Sequence 111, App
c 283	17.2	0.3	39	9	US-10-211-357-36	Sequence 36, Appl	c 356	16.8	0.3	31	10	US-09-801-274-559	Sequence 559, App
c 284	17.2	0.3	39	9	US-10-044-632-242	Sequence 242, Appl	c 357	16.8	0.3	31	10	US-09-801-274-559	Sequence 828, App
c 285	17.2	0.3	39	10	US-09-850-165-14	Sequence 14, Appl	c 358	16.8	0.3	31	10	US-09-801-274-828	Sequence 1093, Ap
c 286	17.2	0.3	40	9	US-09-966-277-29	Sequence 29, Appl	c 359	16.8	0.3	31	10	US-09-801-274-1093	Sequence 580, App
c 287	17.2	0.3	40	9	US-09-966-930-29	Sequence 29, Appl	c 360	16.8	0.3	31	10	US-09-263-959-580	Sequence 26, Appl
c 288	17.2	0.3	40	9	US-09-817-513A-25	Sequence 25, Appl	c 361	16.8	0.3	33	9	US-10-033-300-26	Sequence 25, Appl
c 289	17.2	0.3	40	10	US-09-828-034-1	Sequence 1, Appl	c 362	16.8	0.3	34	9	US-10-194-138-25	Sequence 57, Appl
c 290	17.2	0.3	40	10	US-09-922-146-37	Sequence 37, Appl	c 363	16.8	0.3	35	9	US-09-908-931B-57	Sequence 71, Appl
c 291	17	0.3	20	9	US-09-754-853A-433	Sequence 433, App	c 364	16.8	0.3	36	9	US-09-899-046-71	Sequence 14, Appl
c 292	17	0.3	20	9	US-10-060-830-505	Sequence 505, App	c 365	16.8	0.3	36	9	US-09-876-235-14	Sequence 79, Appl
c 293	17	0.3	25	9	US-09-730-289B-1755	Sequence 1755, Ap	c 366	16.8	0.3	36	9	US-09-878-281-71	Sequence 71, Appl
c 294	17	0.3	25	9	US-09-730-289B-1756	Sequence 1756, Ap	c 367	16.8	0.3	36	9	US-09-977-418-79	Sequence 79, Appl
c 295	17	0.3	25	9	US-09-730-289B-3669	Sequence 3669, Ap	c 368	16.8	0.3	36	9	US-10-022-832-71	Sequence 73, Appl
c 296	17	0.3	25	9	US-09-730-289B-3670	Sequence 3670, Ap	c 369	16.8	0.3	36	9	US-09-977-033A-79	Sequence 79, Appl
c 297	17	0.3	25	10	US-09-866-108-15555	Sequence 15555, A	c 370	16.8	0.3	36	9	US-10-287-919-235	Sequence 235, App
c 298	17	0.3	25	10	US-09-779-881-1	Sequence 1, Appl	c 371	16.8	0.3	36	10	US-09-057-351-14	Sequence 14, Appl
c 299	17	0.3	26	10	US-09-779-881-1	Sequence 1, Appl	c 372	16.8	0.3	36	10	US-09-923-246-30	Sequence 30, Appl
c 300	17	0.3	27	9	US-09-232-785-359	Sequence 359, App	c 373	16.8	0.3	36	10	US-09-825-561A-21	Sequence 21, Appl
c 301	17	0.3	27	9	US-10-085-906-78	Sequence 78, Appl	c 374	16.8	0.3	36	10	US-09-931-209-78	Sequence 78, Appl
c 302	17	0.3	27	10	US-09-817-014-51	Sequence 51, Appl	c 375	16.8	0.3	37	9	US-09-232-785-358	Sequence 358, App
c 303	17	0.3	27	10	US-09-808-212A-23	Sequence 23, Appl	c 376	16.8	0.3	37	9	US-09-848-754A-6120	Sequence 6120, Ap
c 304	17	0.3	30	9	US-09-984-842-3	Sequence 3, Appl	c 377	16.8	0.3	37	9	US-09-776-474-1936	Sequence 1936, Ap
c 305	17	0.3	30	9	US-09-912-263-105	Sequence 105, App	c 378	16.8	0.3	37	9	US-10-123-071-4	Sequence 4, Appl
c 306	17	0.3	31	10	US-09-801-274-848	Sequence 848, App	c 379	16.8	0.3	37	12	US-10-038-984-13	Sequence 13, Appl
c 307	17	0.3	31	10	US-09-801-274-1234	Sequence 1234, Ap	c 380	16.8	0.3	38	9	US-09-793-139-42	Sequence 42, Appl
c 308	17	0.3	31	10	US-09-801-274-1561	Sequence 1561, Ap	c 381	16.8	0.3	38	9	US-09-793-139-43	Sequence 43, Appl
c 309	17	0.3	31	10	US-09-801-274-1561	Sequence 14, Appl	c 382	16.8	0.3	38	9	US-09-733-042-3	Sequence 3, Appl
c 310	17	0.3	33	9	US-09-006-298-14	Sequence 4, Appl	c 383	16.8	0.3	38	9	US-09-733-042-3	Sequence 1424, Ap
c 311	17	0.3	34	10	US-09-950-902-5	Sequence 5, Appl	c 384	16.8	0.3	38	9	US-09-825-805-1424	Sequence 1424, Ap

385 16.8 0.3 38 9 US-09-780-533A-3480 Sequence 3480, Ap  
c 386 16.8 0.3 38 9 US-09-780-533A-3629 Sequence 3629, Ap  
c 387 16.8 0.3 38 9 US-09-780-533A-3851 Sequence 3851, Ap  
c 388 16.8 0.3 38 9 US-09-780-533A-3908 Sequence 3908, Ap  
c 389 16.8 0.3 38 9 US-09-776-474-1541 Sequence 1541, Ap  
c 390 16.8 0.3 38 9 US-09-780-164-1186 Sequence 1186, Ap  
c 391 16.8 0.3 38 9 US-09-780-164-1575 Sequence 1575, Ap  
c 392 16.8 0.3 38 10 US-09-818-879-43 Sequence 43, Appl  
c 393 16.8 0.3 38 10 US-09-818-879-43 Sequence 43, Appl  
c 394 16.8 0.3 38 10 US-09-211-755B-42 Sequence 42, Appl  
c 395 16.8 0.3 38 10 US-09-211-755B-43 Sequence 43, Appl  
c 396 16.8 0.3 39 9 US-09-963-667-3 Sequence 3, Appl  
c 397 16.8 0.3 39 9 US-09-991-262-9 Sequence 9, Appl  
c 398 16.8 0.3 39 9 US-10-134-138-30 Sequence 30, Appl  
c 399 16.8 0.3 39 10 US-09-756-250B-5 Sequence 5, Appl  
c 400 16.8 0.3 39 10 US-09-963-667-15 Sequence 15, Appl  
c 401 16.8 0.3 40 9 US-09-963-667-16 Sequence 16, Appl  
c 402 16.8 0.3 40 9 US-09-963-667-17 Sequence 17, Appl  
c 403 16.8 0.3 40 9 US-09-963-667-18 Sequence 18, Appl  
c 404 16.8 0.3 40 9 US-09-963-667-19 Sequence 19, Appl  
c 405 16.8 0.3 40 9 US-10-135-965-17 Sequence 17, Appl  
c 406 16.8 0.3 40 9 US-10-135-965-18 Sequence 18, Appl  
c 407 16.8 0.3 40 9 US-10-135-965-27 Sequence 27, Appl  
c 408 16.8 0.3 40 9 US-10-135-965-61 Sequence 61, Appl  
c 409 16.8 0.3 40 9 US-09-997-977-17 Sequence 17, Appl  
c 410 16.6 0.3 23 9 US-09-970-820-10 Sequence 10, Appl  
c 411 16.6 0.3 23 9 US-09-986-718-10 Sequence 10, Appl  
c 412 16.6 0.3 23 10 US-09-371-900-10 Sequence 10, Appl  
c 413 16.6 0.3 24 9 US-10-137-788-16 Sequence 16, Appl  
c 414 16.6 0.3 24 12 US-10-066-151-90 Sequence 90, Appl  
c 415 16.6 0.3 25 9 US-10-060-830-509 Sequence 509, Appl  
c 416 16.6 0.3 25 9 US-09-730-289B-1753 Sequence 1753, Ap  
c 417 16.6 0.3 25 9 US-09-730-289B-1754 Sequence 1754, Ap  
c 418 16.6 0.3 25 9 US-09-730-289B-3667 Sequence 3667, Ap  
c 419 16.6 0.3 25 9 US-09-730-289B-3668 Sequence 3668, Ap  
c 420 16.6 0.3 25 9 US-10-215-112-2205 Sequence 2205, Ap  
c 421 16.6 0.3 25 9 US-10-215-112-8451 Sequence 8451, Ap  
c 422 16.6 0.3 25 10 US-09-866-108-3885 Sequence 3885, Ap  
c 423 16.6 0.3 25 10 US-09-965-602-32 Sequence 32, Appl  
c 424 16.6 0.3 27 10 US-09-841-833-5 Sequence 5, Appl  
c 425 16.6 0.3 28 9 US-09-799-462A-4 Sequence 4, Appl  
c 426 16.6 0.3 28 9 US-10-125-767-4 Sequence 4, Appl  
c 427 16.6 0.3 28 9 US-09-836-911A-4 Sequence 4, Appl  
c 428 16.6 0.3 28 9 US-10-151-081-4 Sequence 4, Appl  
c 429 16.6 0.3 28 9 US-10-024-648-17 Sequence 17, Appl  
c 430 16.6 0.3 28 10 US-10-024-648-18 Sequence 18, Appl  
c 431 16.6 0.3 30 9 US-09-096-648-4 Sequence 4, Appl  
c 432 16.6 0.3 30 9 US-10-010-920-42 Sequence 42, Appl  
c 433 16.6 0.3 30 9 US-09-957-483-1 Sequence 1, Appl  
c 434 16.6 0.3 30 9 US-09-849-199A-11 Sequence 11, Appl  
c 435 16.6 0.3 30 9 US-10-008-721-42 Sequence 42, Appl  
c 436 16.6 0.3 31 9 US-09-903-456-115 Sequence 115, Appl  
c 437 16.6 0.3 31 9 US-09-726-258-40 Sequence 40, Appl  
c 438 16.6 0.3 31 9 US-09-778-900A-12 Sequence 12, Appl  
c 439 16.6 0.3 31 9 US-09-780-533A-5093 Sequence 40, Appl  
c 440 16.6 0.3 31 10 US-09-801-274-138 Sequence 5150, Ap  
c 441 16.6 0.3 31 10 US-09-801-274-138 Sequence 138, Appl  
c 442 16.6 0.3 31 10 US-09-801-274-138 Sequence 600, Appl  
c 443 16.6 0.3 31 10 US-09-801-274-138 Sequence 444, Appl  
c 444 16.6 0.3 33 9 US-09-765-272-444 Sequence 6, Appl  
c 445 16.6 0.3 33 9 US-09-800-632A-6 Sequence 75, Appl  
c 446 16.6 0.3 33 9 US-09-999-724-75 Sequence 43, Appl  
c 447 16.6 0.3 33 9 US-10-083-168-43 Sequence 43, Appl  
c 448 16.6 0.3 33 9 US-10-083-168-43 Sequence 44, Appl  
c 449 16.6 0.3 33 9 US-10-194-138-21 Sequence 21, Appl  
c 450 16.6 0.3 33 10 US-10-199-881-37 Sequence 37, Appl  
c 451 16.6 0.3 33 10 US-09-757-992-4 Sequence 4, Appl  
c 452 16.6 0.3 33 10 US-09-842-883-5 Sequence 5, Appl  
c 453 16.6 0.3 34 9 US-10-201-310-11 Sequence 825, Appl  
c 454 16.6 0.3 34 9 US-10-201-310-11 Sequence 11, Appl  
c 455 16.6 0.3 34 9 US-10-194-138-7 Sequence 7, Appl  
c 456 16.6 0.3 34 10 US-10-194-138-29 Sequence 29, Appl  
c 457 16.6 0.3 35 9 US-09-263-959-711 Sequence 711, Appl  
c 458 16.6 0.3 35 9 US-10-085-906-354 Sequence 354, Appl  
c 459 16.6 0.3 35 9 US-10-195-752-29 Sequence 29, Appl  
c 460 16.6 0.3 35 9 US-09-093-972C-981 Sequence 981, Appl  
c 461 16.6 0.3 36 9 US-10-268-133-5 Sequence 5, Appl  
c 462 16.6 0.3 36 9 US-09-900-379-113 Sequence 113, Appl  
c 463 16.6 0.3 36 9 US-10-118-100-3 Sequence 3, Appl  
c 464 16.6 0.3 36 10 US-10-246-581-15 Sequence 15, Appl  
c 465 16.6 0.3 36 10 US-09-848-164-113 Sequence 113, Appl  
c 466 16.6 0.3 37 9 US-09-833-654-6 Sequence 6, Appl  
c 467 16.6 0.3 37 9 US-09-864-785-1897 Sequence 1897, Ap  
c 468 16.6 0.3 37 9 US-09-851-486-89 Sequence 89, Appl  
c 469 16.6 0.3 37 9 US-09-851-486-90 Sequence 90, Appl  
c 470 16.6 0.3 37 9 US-09-851-486-91 Sequence 91, Appl  
c 471 16.6 0.3 37 9 US-09-851-486-92 Sequence 92, Appl  
c 472 16.6 0.3 37 9 US-09-851-486-93 Sequence 93, Appl  
c 473 16.6 0.3 37 9 US-09-851-486-94 Sequence 94, Appl  
c 474 16.6 0.3 37 9 US-09-851-486-95 Sequence 95, Appl  
c 475 16.6 0.3 37 9 US-09-848-754A-6334 Sequence 6334, Ap  
c 476 16.6 0.3 37 9 US-09-848-754A-6452 Sequence 6452, Ap  
c 477 16.6 0.3 37 10 US-10-139-480-3 Sequence 3, Appl  
c 478 16.6 0.3 37 10 US-09-263-959-743 Sequence 743, Appl  
c 479 16.6 0.3 37 10 US-09-263-959-801 Sequence 801, Appl  
c 480 16.6 0.3 38 9 US-09-263-959-815 Sequence 815, Appl  
c 481 16.6 0.3 38 9 US-09-851-486-83 Sequence 83, Appl  
c 482 16.6 0.3 38 9 US-10-028-392-62 Sequence 62, Appl  
c 483 16.6 0.3 38 10 US-09-780-164-1287 Sequence 1287, Ap  
c 484 16.6 0.3 39 9 US-09-120-044-13 Sequence 13, Appl  
c 485 16.6 0.3 39 9 US-10-023-530-14 Sequence 14, Appl  
c 486 16.6 0.3 39 9 US-10-287-919-1781 Sequence 1781, Ap  
c 487 16.6 0.3 39 10 US-09-988-899-64 Sequence 2497, Ap  
c 488 16.6 0.3 40 9 US-09-966-546-34 Sequence 64, Appl  
c 489 16.6 0.3 40 9 US-09-966-545-34 Sequence 34, Appl  
c 490 16.6 0.3 40 9 US-09-965-212-34 Sequence 34, Appl  
c 491 16.6 0.3 40 9 US-10-228-070-13 Sequence 13, Appl  
c 492 16.6 0.3 40 9 US-09-981-803-38 Sequence 38, Appl  
c 493 16.6 0.3 40 10 US-09-245-802-80 Sequence 80, Appl  
c 494 16.6 0.3 40 10 US-09-350-874-44 Sequence 44, Appl  
c 495 16.6 0.3 40 10 US-09-910-635-1 Sequence 1, Appl  
c 496 16.6 0.3 40 10 US-09-956-412-1 Sequence 1, Appl  
c 497 16.6 0.3 40 10 US-09-263-959-458 Sequence 458, Appl  
c 498 16.6 0.3 40 12 US-10-046-722-13 Sequence 13, Appl  
c 499 16.4 0.3 18 9 US-10-011-204-1 Sequence 1, Appl  
c 500 16.4 0.3 18 9 US-10-011-204-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-10-085-906-27/c  
; Sequence 27, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343C2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens

\_\_\_\_\_

## RESULT 5

US-09-263-959-665/c  
; Sequence 665, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 665:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-665

Query Match 0.5%; Score 24.2; DB 10; Length 29;  
Best Local Similarity 89.7%; Pred. No. 1.3e+04;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACAC 2338

Db 29 CACACACACACACACACACACACACAC 1

## RESULT 6

US-09-920-342-9/c  
; Sequence 9, Application US/09920342  
; Patent No. US20020137709A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Southern California  
; APPLICANT: Lin, Shi-Lung  
; APPLICANT: Chuong, Cheng-Ming  
; APPLICANT: Widelitz, Randall B.  
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS  
; FILE REFERENCE: 13761-7024  
; CURRENT APPLICATION NUMBER: US/09/920,342  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 60/222,479  
; PRIOR FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

US-09-920-342-9/c  
; Sequence 9, Application US/09920342  
; Patent No. US20020137709A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Southern California  
; APPLICANT: Lin, Shi-Lung  
; APPLICANT: Chuong, Cheng-Ming  
; APPLICANT: Widelitz, Randall B.  
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS  
; FILE REFERENCE: 13761-7024  
; CURRENT APPLICATION NUMBER: US/09/920,342  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 60/222,479  
; PRIOR FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Anti-bcl2 primer  
US-09-920-342-9

Query Match 0.5%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2725 CCATGCCCTCCCTGGCCTGAAGAAG 2748

Db 24 CCATGCCCTCCCTGGCCTGAAGAAG 1

## RESULT 7

US-09-920-342-11  
; Sequence 11, Application US/09920342  
; Patent No. US20020137709A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Southern California  
; APPLICANT: Lin, Shi-Lung  
; APPLICANT: Chuong, Cheng-Ming  
; APPLICANT: Widelitz, Randall B.  
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS  
; FILE REFERENCE: 13761-7024  
; CURRENT APPLICATION NUMBER: US/09/920,342  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: US 60/222,479  
; PRIOR FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: bcl2 primer  
US-09-920-342-11

Query Match 0.5%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1985 GGATGACTGAGTACCTGAACCGGC 2008

Db 1 GGATGACTGAGTACCTGAACCGGC 24

## RESULT 8

US-09-735-363A-1/c  
; Sequence 1, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 1  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-1

Query Match 0.5%; Score 23.8; DB 10; Length 27;  
Best Local Similarity 92.6%; Pred. No. 1.6e+04;

us-09-375-514-19.rnpb

Sun Jun 1 14:55:56 2003

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACAC 2336  
 ||||| ||| ||||| |||||  
 Db 27 CACACACACACACACACACACAC 1

RESULT 9

US-09-735-363A-5/c  
 ; Sequence 5, Application US/09735363A  
 ; Patent No. US20010041681A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fillion, Mario  
 ; APPLICANT: Phillip, Nigel  
 ; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 ; FILE REFERENCE: 02811-0181  
 ; CURRENT APPLICATION NUMBER: US/09/735,363A  
 ; PRIOR FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/170,325  
 ; PRIOR FILING DATE: 1999-12-13  
 ; PRIOR APPLICATION NUMBER: 60/228,925  
 ; PRIOR FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide  
 US-09-735-363A-5

Query Match 0.5%; Score 23.8; DB 10; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 1.6e+04;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACAC 2337  
 ||||| ||| ||||| |||||  
 Db 27 ACACACACACACACACACACAC 1

RESULT 10

US-09-735-363A-66/c  
 ; Sequence 66, Application US/09735363A  
 ; Patent No. US20010041681A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fillion, Mario  
 ; APPLICANT: Phillip, Nigel  
 ; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 ; FILE REFERENCE: 02811-0181  
 ; CURRENT APPLICATION NUMBER: US/09/735,363A  
 ; PRIOR FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/170,325  
 ; PRIOR FILING DATE: 1999-12-13  
 ; PRIOR APPLICATION NUMBER: 60/228,925  
 ; PRIOR FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 66  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide  
 US-09-735-363A-66

Query Match 0.5%; Score 23.8; DB 10; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 1.6e+04;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACAC 2336  
 ||||| ||| ||||| |||||  
 Db 27 CACACACACACACACACACAC 1

RESULT 11

US-09-263-959-770/c  
 ; Sequence 770, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hood, Leroy E.  
 ; APPLICANT: Rowen, Lee  
 ; APPLICANT: Koop, Ben F.  
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U  
 ; NUMBER OF SEQUENCES: 1279  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/263,959  
 ; FILING DATE: 05-MAR-1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 920010.426C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 770:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-09-263-959-770

Query Match 0.5%; Score 23.8; DB 10; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 1.6e+04;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACAC 2337  
 ||||| ||| ||||| |||||  
 Db 27 ACACACACACACACACACACAC 1

RESULT 12

US-09-263-959-600/c  
 ; Sequence 600, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hood, Leroy E.  
 ; APPLICANT: Rowen, Lee  
 ; APPLICANT: Koop, Ben F.  
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH  
 ; NUMBER OF SEQUENCES: 1279  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS



ISEX: 06141 PENNIE  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO

US-09-371-900-11/c  
Sequence 11, Application US/09371900  
Patent No. US20020137700A1  
GENERAL INFORMATION:



us-09-375-514-19.rnpb

Sun Jun 1 14:55:56 2003

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide primers  
US-09-931-732-21

Query Match 0.4%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1722 GGTGCCACCTGTGTCCACCTG 1743  
Db 1 GGTGCCACCTGTGTCCACCTG 22

RESULT 17

US-09-925-674A-1  
Sequence 1, Application US/09925674A  
Patent No. US20020119943A1  
GENERAL INFORMATION:  
APPLICANT: AMRAD Operations Pty Ltd  
TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
FILE REFERENCE: 11686a  
CURRENT APPLICATION NUMBER: US/09/925,674A  
CURRENT FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/925,674  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: PN8965  
PRIOR FILING DATE: 1996-03-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 16  
OTHER INFORMATION: n is inosine  
NAME/KEY: modified\_base  
LOCATION: 19  
OTHER INFORMATION: n is inosine  
NAME/KEY: modified\_base  
LOCATION: 22  
OTHER INFORMATION: n is inosine  
NAME/KEY: modified\_base  
LOCATION: 25  
OTHER INFORMATION: n is inosine  
US-09-925-674A-1

Query Match 0.4%; Score 21.4; DB 10; Length 33;  
Best Local Similarity 74.1%; Pred. No. 7.6e+04; 4; Indels 0; Gaps 0;  
Matches 20; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1884 GAACGGGGGAGGAGTGTGGCTTCTT 1910  
Db 7 GAACGGGGGAGGAGTGTGGCTTCTT 33

RESULT 18

US-10-231-381-27  
Sequence 27, Application US/10231381  
Publication No. US20030096277A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Xiangning  
TITLE OF INVENTION: ALLELE SPECIFIC PCR FOR GENOTYPING  
FILE REFERENCE: 02940201aa  
CURRENT APPLICATION NUMBER: US/10/231,381  
CURRENT FILING DATE: 2002-08-30

APPLICANT: FALLB, DEAN A  
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESS: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/371,900  
FILING DATE: 11-Aug-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-104  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-371-900-11

Query Match 0.4%; Score 22.4; DB 10; Length 24;  
Best Local Similarity 95.8%; Pred. No. 3.4e+04;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1875 GGACGGGCTGAACCTGGGGGAGGAT 1898  
Db 24 GGATGGGCTGAACCTGGGGGAGGAT 1

RESULT 16

US-09-931-732-21  
Sequence 21, Application US/09931732  
Publication No. US20030045488A1  
GENERAL INFORMATION:  
APPLICANT: Brown, Bob D.  
APPLICANT: Riley, Timothy A.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING  
TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES  
FILE REFERENCE: OASBIO.001C1  
CURRENT APPLICATION NUMBER: US/09/931,732  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US00/09293  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: US 60/128,377  
PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 30

; PRIOR APPLICATION NUMBER: 60/315,776  
; CURRENT FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide primer  
US-10-231-381-27

Query Match 0.4%; Score 21.2; DB 9; Length 39;  
Best Local Similarity 76.5%; Pred. No. 9.2e+04;  
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2300 ATATAACATCACACACACACACACACACACA 2333  
Db 3 ATACAATTTCACACACACCCACGCGTCAACCCACA 36

## RESULT 19

US-09-925-674A-3/c  
; Sequence 3, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: P88965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 14  
; OTHER INFORMATION: n is inosine  
; NAME/KEY: modified\_base  
; LOCATION: 17  
; OTHER INFORMATION: n is inosine  
; NAME/KEY: modified\_base  
; LOCATION: 20  
; OTHER INFORMATION: n is inosine  
US-09-925-674A-3

Query Match 0.4%; Score 21; DB 10; Length 31;  
Best Local Similarity 80.8%; Pred. No. 9.2e+04;  
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2020 TGGATCCAGGATACCGAGGCTGGGA 2045  
Db 31 TGGATCCAGGATACCGAGGCTGGGA 6

## RESULT 20

US-09-829-631A-3/c  
; Sequence 3, Application US/09829631A  
; Patent No. US20020091235A1  
; GENERAL INFORMATION:  
; APPLICANT: Sibley, David R.  
; APPLICANT: Monsma, Frederick J.  
; APPLICANT: Hamblin, Mark  
; TITLE OF INVENTION: The ST-B17 Serotonin Receptor  
; FILE REFERENCE: NIH047.1Cp1C1

; CURRENT APPLICATION NUMBER: US/09/829,631A  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 08/428,242  
; PRIOR FILING DATE: 1995-09-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-829-631A-3

Query Match 0.4%; Score 21; DB 10; Length 33;  
Best Local Similarity 82.8%; Pred. No. 9.6e+04;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4497 GGCTGCTCTTCAGGCTCTCTGAAATGC 4525  
Db 31 GGCTGCTCTTCAGGCTCTCTGCTATGC 3

## RESULT 21

US-09-764-891-10175/c  
; Sequence 10175, Application US/09764891  
; Publication No. US20030077808A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: EC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10175  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-891-10175

Query Match 0.4%; Score 21; DB 9; Length 30;  
Best Local Similarity 73.0%; Pred. No. 1.1e+05;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1126 GCACCTGATTTTACTATTAGTTGTTTCTTT 1162  
Db 38 GCATTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

## RESULT 22

US-10-112-653-1012/c  
; Sequence 1012, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Daniel J.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1012  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide

us-09-375-514-19.rnpb

Sun Jun 1 14:55:56 2003

Db 24 CACACACACACACACACACACA 1

US-10-112-653-1012

Query Match 0.4%; Score 20.8; DB 9; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e+04;  
Matches 22; Conservative 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333  
Db 24 CACACACACACACACACACACA 1

RESULT 23  
US-10-017-995-1068/c  
; Sequence 1068, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1068  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-1068

Query Match 0.4%; Score 20.8; DB 9; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e+04;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333  
Db 24 CACACACACACACACACACACA 1

RESULT 24  
US-09-776-479-1068/c  
; Sequence 1068, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1068  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-1068

Query Match 0.4%; Score 20.8; DB 9; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e+04;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333

Db 24 CACACACACACACACACACACA 1

RESULT 25  
US-09-735-363A-21/c  
; Sequence 21, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-21

Query Match 0.4%; Score 20.8; DB 10; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e+04;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACA 2333  
Db 24 CACACACACACACACACACACA 1

RESULT 26  
US-09-735-363A-22/c  
; Sequence 22, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-22

Query Match 0.4%; Score 20.8; DB 10; Length 24;  
Best Local Similarity 91.7%; Pred. No. 8.6e+04;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACAC 2334  
Db 24 ACACACACACACACACACACAC 1

RESULT 27  
US-10-085-906-189/c

```
; Sequence 189, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-189
```

```
Query Match 0.4%; Score 20.8; DB 9; Length 34;
Best Local Similarity 78.1%; Pred. No. 1.1e+05;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2312 CACACACAGACAGACACACACACACAA 2343
DB 34 CAAACAAACACACACACACACACAAACAAAA 3
```

```
RESULT 28
US-09-931-732-22/g
; Sequence 22, Application US/09931732
; Publication No. US20030045488A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
; FILE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
; FILE REFERENCE: OASBIO 001C1
; CURRENT APPLICATION NUMBER: US/09/931,732
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09293
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,377
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-931-732-22
```

```
Query Match 0.4%; Score 20.4; DB 9; Length 22;
Best Local Similarity 95.5%; Pred. No. 1e+05;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2159 CCTATCTGAGCCCAAGTGAAG 2180
DB 22 CCTATCTGGGCCCAAGTGAAG 1
```

```
RESULT 29
US-09-949-305B-10/c
; Sequence 10, Application US/09949305B
; Publication No. US20030022318A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Ying, Shao-Yao
; TITLE OF INVENTION: Method for Thermocycling Amplification of Nucleic Acid Sequences
; FILE OF INVENTION: Generation of Related Peptides Thereof
; FILE REFERENCE: 265/014
; CURRENT APPLICATION NUMBER: US/09/949,305B
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/494,212
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense bcl-2 primer
US-09-949-305B-10
```

```
Query Match 0.4%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2729 GCTCCCTGGCTGAAGAG 2748
DB 20 GCTCCCTGGCTGAAGAG 1
```

```
RESULT 30
US-09-972-469-25
; Sequence 25, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Fang
; APPLICANT: Zhou, Daixing
; TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDE
; FILE OF INVENTION: EUKARYOTIC ORGANISMS FOR DNA ARRAYS
; FILE REFERENCE: SP01-290
; CURRENT APPLICATION NUMBER: US/09/972,469
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-469-25
```

```
Query Match 0.4%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2783 TGGTGGGAGGAAAAGATTG 2802
DB 1 TGGTGGGAGGAAAAGATTG 20
```

```
RESULT 31
US-09-817-387-11/c
; Sequence 11, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
```

; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotides, linkages between positions 1  
; OTHER INFORMATION: to 20 are phosphorothioate, linkages between  
; OTHER INFORMATION: positions 20 to 28 are N3' to N5'  
; OTHER INFORMATION: phosphoramidates  
; OTHER INFORMATION: position 28 is modified by a 3'-aminodeoxyriboseyl  
; OTHER INFORMATION: residue  
US-09-817-387-11

Query Match 0.4%; Score 20; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.5e+05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1880 GGTGAAGTGGGGGAGGATT 1899  
Db 20 GGTGAAGTGGGGGAGGATT 1

RESULT 32  
US-09-801-274-1526/c  
; Sequence 1526, Application US/09801274  
; Patent No. US2002032319A1  
; GENERAL INFORMATION:  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Lander, Eric S.  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
; FILE REFERENCE: 2825.2009-001  
; CURRENT APPLICATION NUMBER: US/09/801,274  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/187,510  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 60/206,129  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 1802  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1526  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-274-1526

Query Match 0.4%; Score 20; DB 10; Length 31;  
Best Local Similarity 90.9%; Pred. No. 1.6e+05;  
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 73 CGTGGCGCGCGCGCGTGGC 94  
Db 22 CGCTGCGCGCGCGCGTGGC 1

RESULT 33  
US-09-864-785-1826  
; Sequence 1826, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of NF-kappa B  
; FILE REFERENCE: 400/022 (MEH00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1826  
; LENGTH: 37

; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid  
US-09-864-785-1826

Query Match 0.4%; Score 20; DB 9; Length 37;  
Best Local Similarity 69.4%; Pred. No. 1.9e+05;  
Matches 25; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 162 CGGAGGTCGGGAGGCGACCTAGTCGCGCCGCCG 197  
Db 2 CGGAGGCGCGAAAGCGGAGGAGGUCGCGCCGAG 37

RESULT 34  
US-09-263-959-774  
; Sequence 774, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 774:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-774

Query Match 0.4%; Score 19.8; DB 10; Length 23;  
Best Local Similarity 91.3%; Pred. No. 1.5e+05;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2313 ACACACAGACACACACACACA 2335  
Db 1 ACACACACACATACACACACACA 23

RESULT 35  
US-10-085-906-324/c  
; Sequence 324, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 324  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-324

Query Match 0.4%; Score 19.8; DB 9; Length 32;  
Best Local Similarity 77.4%; Pred. No. 1.9e+05;  
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2313 ACACACAGACACACACACACACACAA 2343  
| | | | | | | | | | | | | | | | | | | | | |  
Db 32 AAAACAAACACACACACACACACACAAAA 2

RESULT 36  
US-09-923-327-60  
; Sequence 60, Application US/09923327  
; Publication No. US20030096236A1  
; GENERAL INFORMATION:  
; APPLICANT: MURPHY, Patricia D.  
; TITLE OF INVENTION: Determining Common Functional Alleles in a Population and Uses Th  
; FILE REFERENCE: 044921-5054-02  
; CURRENT APPLICATION NUMBER: US/09/923,327  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 08/598,591  
; PRIOR FILING DATE: 1996-02-12  
; PRIOR APPLICATION NUMBER: US 08/798,691  
; PRIOR FILING DATE: 1997-02-12  
; PRIOR APPLICATION NUMBER: US 08/905,772  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: US 09/084,471  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: US 09/129,134  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: US 09/524,794  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 260  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 60  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-923-327-60

Query Match 0.4%; Score 19.6; DB 9; Length 38;  
Best Local Similarity 73.5%; Pred. No. 2.4e+05;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3850 GAATCAGCCTTGAACATTTGATGAACTCTG 3883  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 GAAACAGCTATGACCATTTGTTAGTACTCTG 37

RESULT 37  
US-10-231-381-26  
; Sequence 26, Application US/10231381  
; Publication No. US20030096277A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Xiangning

; TITLE OF INVENTION: ALLELE SPECIFIC PCR FOR GENOTYPING  
; FILE REFERENCE: 02940201aa  
; CURRENT APPLICATION NUMBER: US/10/231,381  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 60/315,776  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide primer  
US-10-231-381-26

Query Match 0.4%; Score 19.6; DB 9; Length 39;  
Best Local Similarity 73.5%; Pred. No. 2.5e+05;  
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2300 ATATAACATCACACACACACACACACACA 2333  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 ATAACAATTTCACACACAGGACGTCACCCACA 36

RESULT 38  
US-09-828-034-12  
; Sequence 12, Application US/09828034  
; Patent No. US20020064771A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhong, Weidong  
; APPLICANT: Hong, Zhi  
; APPLICANT: Ferrari, Eric  
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES  
; FILE REFERENCE: IN01185  
; CURRENT APPLICATION NUMBER: US/09/828,034  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: U.S. 60/195,852  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA  
US-09-828-034-12

Query Match 0.4%; Score 19.4; DB 10; Length 24;  
Best Local Similarity 95.2%; Pred. No. 2e+05;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCGCTGCGCGCGCGCGCCGCC 38  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 CCGCGCGCGCGCGCGCGCGCCGCC 23

RESULT 39  
US-09-966-781A-15/c  
; Sequence 15, Application US/09966781A  
; Publication No. US20030036184A1  
; GENERAL INFORMATION:  
; APPLICANT: SOULARD, PATRICIA  
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR  
; FILE REFERENCE: A0000281US  
; CURRENT APPLICATION NUMBER: US/09/966,781A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP004026837  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15  
 LENGTH: 36  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Primer  
 US-09-966-781A-15

Query Match 0.4%; Score 19.4; DB 9; Length 36;  
 Best Local Similarity 79.3%; Pred. No. 2.6e+05;  
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 70 CGCGCTGCGCGCGCGCGCTGCCAGCG 98  
 ||||| ||||| ||||| ||||| |||||  
 DB 30 CGCGCTGCGCGCGCGCGCTGCCAGCG 2

RESULT 40  
 US-09-772-656-3  
 ; Sequence 3, Application US/09772656  
 ; Patent No. US20010049832A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bruce, Wesley B.  
 ; TITLE OF INVENTION: Root Transcriptional Factor  
 ; FILE REFERENCE: 1167R  
 ; CURRENT APPLICATION NUMBER: US/09/772,656  
 ; CURRENT FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/178,916  
 ; PRIOR FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: US Unknown  
 ; PRIOR FILING DATE: 2001-01-19  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-09-772-656-3

Query Match 0.4%; Score 19.2; DB 10; Length 27;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+05;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 194 GCCGCGCAGGACCGAGGAGGAG 217  
 || ||||| ||||| ||||| |||||  
 DB 4 GCTGCGCAGGACCGAGGAGGAG 27

RESULT 41  
 US-09-772-656-7  
 ; Sequence 7, Application US/09772656  
 ; Patent No. US20010049832A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bruce, Wesley B.  
 ; TITLE OF INVENTION: Root Transcriptional Factor  
 ; FILE REFERENCE: 1167R  
 ; CURRENT APPLICATION NUMBER: US/09/772,656  
 ; CURRENT FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/178,916  
 ; PRIOR FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: US Unknown  
 ; PRIOR FILING DATE: 2001-01-19  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-09-772-656-7

Query Match 0.4%; Score 19.2; DB 10; Length 27;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+05;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 194 GCCGCGCAGGACCGAGGAGGAG 217  
 || ||||| ||||| ||||| |||||  
 DB 4 GCTGCGCAGGACCGAGGAGGAG 27

RESULT 42  
 US-09-772-656-11  
 ; Sequence 11, Application US/09772656  
 ; Patent No. US20010049832A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bruce, Wesley B.  
 ; TITLE OF INVENTION: Root Transcriptional Factor  
 ; FILE REFERENCE: 1167R  
 ; CURRENT APPLICATION NUMBER: US/09/772,656  
 ; CURRENT FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/178,916  
 ; PRIOR FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: US Unknown  
 ; PRIOR FILING DATE: 2001-01-19  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 11  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-09-772-656-11

Query Match 0.4%; Score 19.2; DB 10; Length 27;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+05;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 194 GCCGCGCAGGACCGAGGAGGAG 217  
 || ||||| ||||| ||||| |||||  
 DB 4 GCTGCGCAGGACCGAGGAGGAG 27

RESULT 43  
 US-10-133-205-3/c  
 ; Sequence 3, Application US/10133205  
 ; Publication No. US20030024012A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abdenebi-Najar, Latifa  
 ; APPLICANT: Bakker, Hendrikus A.C.  
 ; APPLICANT: Bosch, Hendrik J.  
 ; APPLICANT: Dirnberger, Dietmar  
 ; APPLICANT: Remy, Jean-Jacques  
 ; APPLICANT: Steinkellner, Herta  
 ; APPLICANT: van de Wiel, Dirk F.M.  
 ; TITLE OF INVENTION: GONADOTROPINS IN PLANTS  
 ; FILE REFERENCE: 05032-00019  
 ; CURRENT APPLICATION NUMBER: US/10/133,205  
 ; CURRENT FILING DATE: 2002-04-26  
 ; PRIOR APPLICATION NUMBER: PCT/NL00/00774  
 ; PRIOR FILING DATE: 2000-10-26  
 ; PRIOR APPLICATION NUMBER: EP 99203523.0  
 ; PRIOR FILING DATE: 1999-10-26  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 34  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: amplification primer  
 US-10-133-205-3

Query Match 0.4%; Score 19.2; DB 9; Length 34;  
 Best Local Similarity 87.5%; Pred. No. 2.8e+05;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3582 TCACAAATCCCTAAAGAGGAGCATG 3605  
 ||||| ||||| ||||| ||||| |||||

```
Db 26 TCACAAATCCTAATAGATGCATAG 3
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 172
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-172

Query Match 0.4%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCGCGCCCTCCGCGCGCTGCGCCGCCGCCGCCGCCGCC 38
Db 1 CCGCGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 35

RESULT 47
US-10-112-653-744
; Sequence 744, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 744
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-112-653-744

Query Match 0.4%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCGCGCCCTCCGCGCGCGCTGCGCCGCCGCCGCCGCC 38
Db 1 CCGCGCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 35

RESULT 48
US-10-017-995-771
; Sequence 771, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
```

```
Db 26 TCACAAATCCTAATAGATGCATAG 3
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; TITLE OF INVENTION: AMPLIFICATION PRIMER PAIRS AND USE
; FILE REFERENCE: OASBIO.002C1
; CURRENT APPLICATION NUMBER: US/09/932,129
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US00/09230
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/128,378
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primers
US-09-932-129-1

Query Match 0.4%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1725 GCCACCTGTGGTCCACCTG 1743
Db 1 GCCACCTGTGGTCCACCTG 19

RESULT 45
US-09-992-665-377/C
; Sequence 377, Application US/0992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 377
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-377

Query Match 0.4%; Score 19; DB 9; Length 30;
Best Local Similarity 81.5%; Pred. No. 2.9e+05;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4379 ATGACCAAGCAGATTCATCAATCTATGGTG 4405
Db 28 AGGTCCAGTAGATCCAAATCCATGGTG 2

RESULT 46
US-09-888-326-172
; Sequence 172, Application US/09888326
; Publication No. US20030026801A1
```



```

CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: fastseq for Windows Version 3.0
SEQ ID NO 771
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-10-017-995-771

Query Match          0.4%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 3.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

y      4  CCGGCGCTTCGGCGGCGTGTCCGCCGCCGCCGCC 38
       ||| ||||| ||| ||| ||| ||| ||| |||
       |C|G|C|G|C|G|C|G|C|G|C|G|C|G|C|G|C|

```

```

RESULT 49
US-09-776-479-771
; Sequence 771, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourn, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 771

```

```

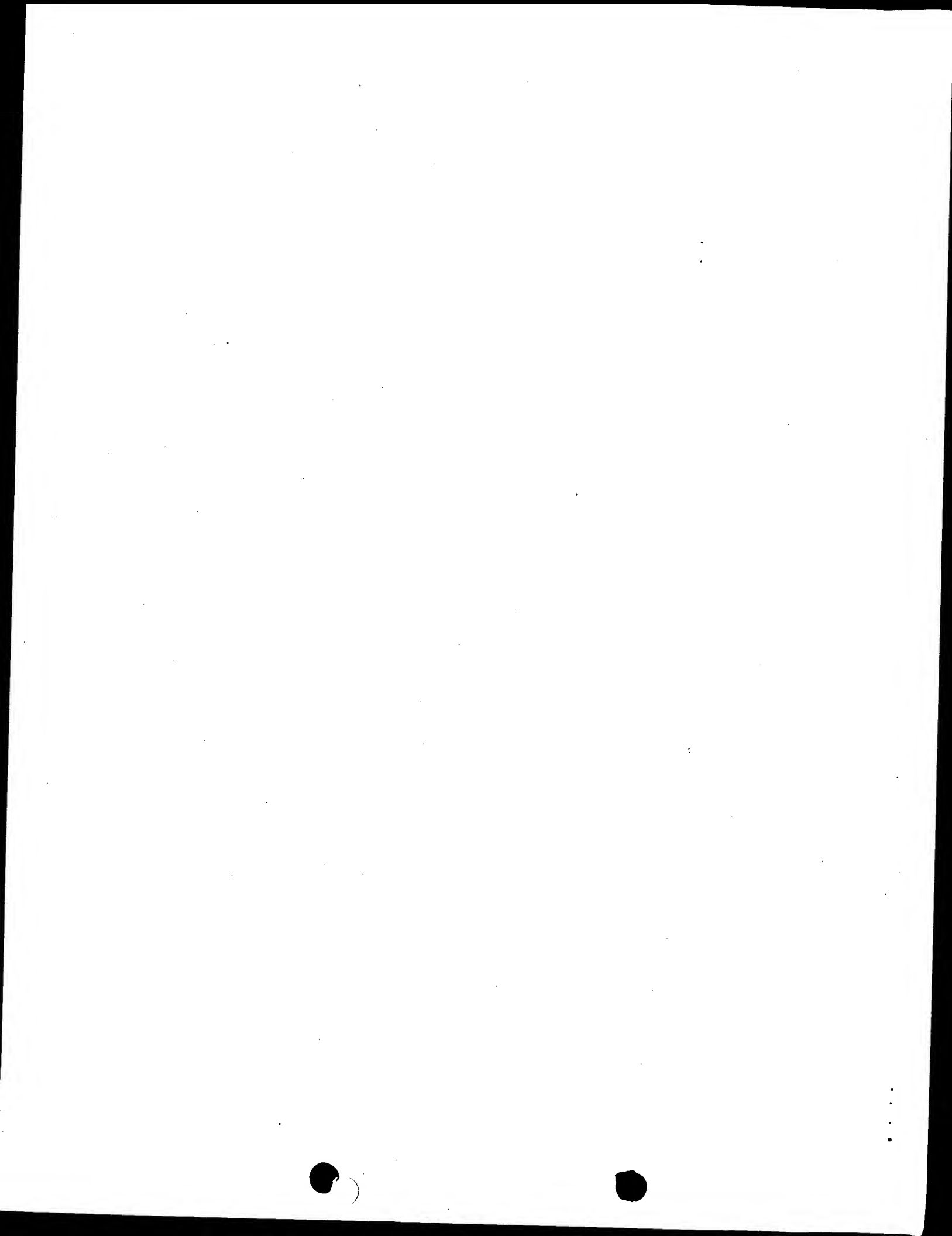
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
DS-09-776-479-771

Query Match      0.4%;      Score 19;  DB 9;  Length 35;
Best Local Similarity 71.4%;  Pred. No. 3.2e+05;
Matches 25;  Conservative 0;  Mismatches 10;  Indels

QY      4  CCGCGCCCTCCGCGCGCGCTGCCGCGCGCGCGCC 38
      | | | | | | | | | | | | | | | | | | | |
pb      1  CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 35

```

RESULT 50  
US-09-932-129--4  
; Sequence 4, Application US/09932129  
; Patent No. US20020119533A1  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Bob D.  
; TITLE OF INVENTION: AMPLIFICATION PRIMER PAIRS AND USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: QASBIO.002C1  
; CURRENT APPLICATION NUMBER: US/09/932.129  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: PCT/US00/09230  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: US 60/128, 378  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 12





101	21	0.4	35	2	US-08-619-542B-9	Sequence 9, Appli	174	19.4	0.4	35	2	US-08-619-542B-12	Sequence 12, Appl
102	21	0.4	35	2	US-08-619-542B-10	Sequence 10, Appl	175	19.4	0.4	35	2	US-08-619-542B-15	Sequence 15, Appl
103	20.8	0.4	24	1	US-08-182-619-3	Sequence 3, Appli	176	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
104	20.8	0.4	24	1	US-08-222-177A-445	Sequence 445, App	c 176	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
105	20.8	0.4	24	1	US-08-330-535A-3	Sequence 3, Appli	c 177	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
106	20.8	0.4	24	1	US-08-838-844-3	Sequence 3, Appli	c 178	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
107	20.8	0.4	24	1	US-08-849-021-2	Sequence 1, Appli	c 179	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
108	20.8	0.4	24	1	US-08-849-021-2	Sequence 1, Appli	c 180	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
109	20.8	0.4	24	1	US-08-849-021-2	Sequence 1, Appli	c 181	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
110	20.6	0.4	27	1	US-08-677-045-10	Sequence 10, Appl	c 182	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
111	20.6	0.4	27	1	US-08-410-804-13	Sequence 13, Appl	c 183	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
112	20.6	0.4	27	1	US-08-607-269-8	Sequence 8, Appli	c 184	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
113	20.6	0.4	27	1	US-08-259-514-13	Sequence 13, Appl	c 185	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
114	20.6	0.4	27	1	US-08-858-311-13	Sequence 13, Appl	c 186	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
115	20.6	0.4	27	1	PCT-US95-04600-8	Sequence 8, Appli	c 187	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
116	20.6	0.4	28	2	US-08-762-106-11	Sequence 11, Appl	c 188	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
117	20.4	0.4	28	2	US-08-320-774-11	Sequence 11, Appl	c 189	19.4	0.4	38	4	US-08-470-369-24	Sequence 24, Appl
118	20.4	0.4	37	2	US-08-360-125-1	Sequence 1, Appli	c 190	19.2	0.4	24	1	US-08-014-943A-6	Sequence 6, Appli
119	20.4	0.4	37	2	US-08-450-578-1	Sequence 1, Appli	c 191	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
120	20.4	0.4	37	2	US-09-017-828-1	Sequence 1, Appli	c 192	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
121	20.4	0.4	37	2	US-09-014-880-1	Sequence 1, Appli	c 193	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
122	20.4	0.4	37	2	US-08-450-363-1	Sequence 1, Appli	c 194	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
123	20.4	0.4	38	4	US-09-459-884-12	Sequence 12, Appl	c 195	19.2	0.4	24	1	US-08-486-421-43	Sequence 43, Appl
124	20.2	0.4	26	5	PCT-US92-10792-44	Sequence 44, Appl	c 196	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
125	20.2	0.4	28	3	US-08-915-609-2	Sequence 2, Appli	c 197	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
126	20.2	0.4	33	1	US-08-068-747-7	Sequence 7, Appli	c 198	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
127	20	0.4	33	6	5478746-1	Patent No. 5478746	c 199	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
128	20	0.4	20	1	US-08-217-082A-1	Sequence 1, Appli	c 200	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
129	20	0.4	20	1	US-08-217-082A-7	Sequence 7, Appli	c 201	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
130	20	0.4	20	1	US-08-405-702A-13	Sequence 13, Appl	c 202	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
131	20	0.4	20	1	US-08-405-702A-14	Sequence 14, Appl	c 203	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
132	20	0.4	20	2	US-08-465-485A-1	Sequence 1, Appli	c 204	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
133	20	0.4	20	2	US-08-465-485A-7	Sequence 7, Appli	c 205	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
134	20	0.4	20	2	US-08-465-485A-26	Sequence 26, Appl	c 206	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
135	20	0.4	20	2	US-08-465-485A-28	Sequence 28, Appl	c 207	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
136	20	0.4	20	3	US-09-080-285-7	Sequence 7, Appli	c 208	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
137	20	0.4	20	3	US-09-080-285-7	Sequence 7, Appli	c 209	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
138	20	0.4	20	3	US-09-080-285-26	Sequence 26, Appl	c 210	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
139	20	0.4	20	3	US-09-080-285-28	Sequence 28, Appl	c 211	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
140	20	0.4	20	4	US-09-445-486-1	Sequence 1, Appli	c 212	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
141	20	0.4	20	4	US-09-445-486-2	Sequence 2, Appli	c 213	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
142	20	0.4	20	4	US-09-445-486-3	Sequence 3, Appli	c 214	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
143	20	0.4	20	4	US-09-445-486-4	Sequence 4, Appli	c 215	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
144	20	0.4	20	4	US-09-378-718-1	Sequence 1, Appli	c 216	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
145	20	0.4	20	4	US-09-724-426-1	Sequence 1, Appli	c 217	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
146	20	0.4	20	4	US-09-724-426-2	Sequence 2, Appli	c 218	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
147	20	0.4	20	4	US-09-724-426-7	Sequence 7, Appli	c 219	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
148	20	0.4	20	4	US-09-724-426-26	Sequence 26, Appl	c 220	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
149	20	0.4	20	4	US-09-724-426-28	Sequence 28, Appl	c 221	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
150	20	0.4	20	4	US-09-301-836-1	Sequence 1, Appli	c 222	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
151	20	0.4	20	4	US-09-301-836-2	Sequence 2, Appli	c 223	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
152	20	0.4	20	4	US-08-798-897-8	Sequence 8, Appli	c 224	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
153	20	0.4	24	2	US-08-978-523-8	Sequence 8, Appli	c 225	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
154	20	0.4	28	1	US-08-390-858B-12	Sequence 12, Appl	c 226	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
155	20	0.4	33	4	US-09-249-585A-11	Sequence 11, Appl	c 227	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
156	19.8	0.4	23	1	US-08-222-177A-454	Sequence 454, App	c 228	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
157	19.8	0.4	23	1	US-08-787-321-22	Sequence 22, Appl	c 229	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
158	19.8	0.4	28	3	US-08-933-008A-2	Sequence 2, Appli	c 230	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
159	19.8	0.4	28	3	US-08-933-008A-3	Sequence 3, Appli	c 231	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
160	19.6	0.4	30	1	US-09-434-131A-4	Sequence 4, Appli	c 232	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
161	19.6	0.4	30	1	US-08-068-747-2	Sequence 2, Appli	c 233	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
162	19.6	0.4	39	4	US-09-425-638A-17	Sequence 17, Appl	c 234	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
163	19.6	0.4	40	1	US-09-543-004-17	Sequence 17, Appl	c 235	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
164	19.4	0.4	21	1	US-08-182-619-4	Sequence 4, Appli	c 236	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
165	19.4	0.4	21	1	US-08-330-535A-4	Sequence 4, Appli	c 237	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
166	19.4	0.4	21	2	US-08-838-844-4	Sequence 4, Appli	c 238	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
167	19.4	0.4	32	1	US-08-126-594-8	Sequence 8, Appli	c 239	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
168	19.4	0.4	32	1	US-08-465-811A-8	Sequence 8, Appli	c 240	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
169	19.4	0.4	32	2	US-08-619-542B-8	Sequence 8, Appli	c 241	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
170	19.4	0.4	35	1	US-08-126-594-12	Sequence 12, Appl	c 242	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
171	19.4	0.4	35	1	US-08-126-594-15	Sequence 15, Appl	c 243	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
172	19.4	0.4	35	1	US-08-465-811A-12	Sequence 12, Appl	c 244	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
173	19.4	0.4	35	1	US-08-465-811A-15	Sequence 15, Appl	c 245	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl
174	19.4	0.4	35	1	US-08-465-811A-15	Sequence 15, Appl	c 246	19.2	0.4	35	1	US-08-126-594-13	Sequence 13, Appl

247	18.8	0.4	35	4	US-09-599-564A-16	Sequence 16, Appl	320	18.2	0.4	39	4	US-09-260-952A-8	Sequence 8, Appl
c 248	18.8	0.4	38	1	US-08-373-124A-635	Sequence 635, App	321	18.2	0.4	39	4	US-09-253-341-8	Sequence 8, Appl
c 249	18.8	0.4	38	1	US-08-435-628-635	Sequence 635, App	322	18.2	0.4	39	4	US-09-253-341A-8	Sequence 8, Appl
250	18.8	0.4	40	1	US-08-484-686B-35	Sequence 35, Appl	323	18.2	0.4	39	4	US-09-337-635-20	Sequence 20, Appl
251	18.8	0.4	40	1	US-08-463-160B-35	Sequence 35, Appl	324	18.2	0.4	39	4	US-09-261-040-8	Sequence 8, Appl
c 252	18.6	0.4	28	3	US-08-863-813A-38	Sequence 38, Appl	325	18.2	0.4	39	4	US-09-097-319A-21	Sequence 21, Appl
c 253	18.6	0.4	28	4	US-08-676-318A-38	Sequence 38, Appl	326	18.2	0.4	39	4	US-09-337-280-20	Sequence 20, Appl
c 254	18.6	0.4	30	1	US-08-467-126-1	Sequence 1, Appl	c 327	18.2	0.4	40	1	US-08-231-342-12	Sequence 12, Appl
c 255	18.6	0.4	30	2	US-08-629-001A-75	Sequence 75, Appl	328	18.2	0.4	40	2	US-08-117-981-11	Sequence 11, Appl
c 256	18.6	0.4	30	2	US-08-476-712-3	Sequence 3, Appl	329	18.2	0.4	40	2	US-08-477-081-11	Sequence 11, Appl
c 257	18.6	0.4	30	4	US-08-642-274D-154	Sequence 154, App	330	18.2	0.4	40	4	US-09-306-290-2	Sequence 2, Appl
c 258	18.6	0.4	34	4	US-09-411-291-3	Sequence 3, Appl	331	18.2	0.4	40	4	US-09-453-195A-10	Sequence 10, Appl
c 259	18.6	0.4	34	1	US-08-434-503-29	Sequence 29, Appl	c 332	18.2	0.4	40	4	US-09-538-709-1236	Sequence 1236, App
c 260	18.6	0.4	35	1	US-08-126-594-20	Sequence 20, Appl	333	18.2	0.4	40	5	PCT-US93-02142-11	Sequence 11, Appl
c 261	18.6	0.4	35	1	US-08-465-811A-20	Sequence 20, Appl	c 334	18	0.4	18	1	US-08-217-082A-17	Sequence 17, Appl
c 262	18.6	0.4	35	2	US-08-619-542B-20	Sequence 20, Appl	c 335	18	0.4	18	2	US-08-465-485A-17	Sequence 17, Appl
c 263	18.6	0.4	40	1	US-08-510-032A-2	Sequence 2, Appl	c 336	18	0.4	18	2	US-08-465-485A-24	Sequence 24, Appl
c 264	18.6	0.4	40	2	US-08-723-306-17	Sequence 17, Appl	337	18	0.4	18	3	US-08-894-784-14	Sequence 14, Appl
c 265	18.6	0.4	40	3	US-08-688-514-2	Sequence 2, Appl	c 338	18	0.4	18	3	US-08-894-784-34	Sequence 34, Appl
c 266	18.6	0.4	40	4	US-09-506-729-5	Sequence 5, Appl	c 339	18	0.4	18	3	US-08-894-784-35	Sequence 35, Appl
c 267	18.6	0.4	40	5	PCT-US96-10041-17	Sequence 17, Appl	c 340	18	0.4	18	3	US-09-080-285-17	Sequence 17, Appl
c 268	18.6	0.4	20	4	US-09-109-663-72	Sequence 72, Appl	c 341	18	0.4	18	3	US-09-080-285-24	Sequence 24, Appl
c 269	18.4	0.4	31	1	US-08-467-126-4	Sequence 4, Appl	c 342	18	0.4	18	3	US-09-249-730-218	Sequence 218, App
c 270	18.4	0.4	31	3	US-08-738-381-24	Sequence 24, Appl	c 343	18	0.4	18	3	US-09-118-220-1	Sequence 1, Appl
c 271	18.4	0.4	35	1	US-07-931-473B-206	Sequence 206, App	c 344	18	0.4	18	4	US-08-738-652-55	Sequence 55, Appl
c 272	18.4	0.4	35	1	US-07-714-131C-206	Sequence 206, App	c 345	18	0.4	18	4	US-09-030-701-27	Sequence 27, Appl
c 273	18.4	0.4	35	1	US-08-412-110-206	Sequence 206, App	c 346	18	0.4	18	4	US-09-286-098-59	Sequence 59, Appl
c 274	18.4	0.4	35	2	US-08-409-442A-206	Sequence 206, App	c 347	18	0.4	18	4	US-09-286-098-59	Sequence 59, Appl
c 275	18.4	0.4	35	2	US-08-469-609A-206	Sequence 206, App	c 348	18	0.4	18	4	US-08-960-098-104	Sequence 104, App
c 276	18.4	0.4	35	3	US-09-143-190-206	Sequence 206, App	c 349	18	0.4	18	4	US-09-078-954-14	Sequence 14, Appl
c 277	18.4	0.4	35	4	US-09-502-344-206	Sequence 206, App	c 350	18	0.4	18	4	US-09-325-193A-51	Sequence 51, Appl
c 278	18.4	0.4	36	1	US-08-093-453B-12	Sequence 12, Appl	c 351	18	0.4	18	4	US-09-724-426-17	Sequence 17, Appl
c 279	18.4	0.4	36	1	US-08-459-041A-9	Sequence 9, Appl	c 352	18	0.4	18	4	US-09-724-426-24	Sequence 24, Appl
c 280	18.4	0.4	36	2	US-08-596-387B-113	Sequence 113, App	c 353	18	0.4	18	4	US-09-191-170-53	Sequence 53, Appl
c 281	18.4	0.4	36	2	US-08-863-639A-31	Sequence 31, Appl	c 354	18	0.4	20	1	US-08-063-167A-59	Sequence 59, Appl
c 282	18.4	0.4	36	4	US-09-067-615-113	Sequence 113, App	355	18	0.4	20	1	US-08-007-997A-59	Sequence 59, Appl
c 283	18.4	0.4	36	4	US-09-462-569B-4	Sequence 4, Appl	356	18	0.4	20	2	US-08-440-740A-59	Sequence 59, Appl
c 284	18.4	0.4	36	5	PCT-US95-09816A-113	Sequence 113, App	357	18	0.4	20	2	US-08-344-155C-59	Sequence 59, Appl
c 285	18.4	0.4	37	1	US-08-113-646A-44	Sequence 44, Appl	358	18	0.4	20	3	US-08-982-845B-59	Sequence 59, Appl
c 286	18.4	0.4	40	2	US-08-771-624B-1	Sequence 1, Appl	359	18	0.4	20	3	US-08-991-525B-59	Sequence 59, Appl
c 287	18.4	0.4	40	2	US-08-440-209-4	Sequence 4, Appl	360	18	0.4	20	3	US-09-085-759-59	Sequence 59, Appl
c 288	18.4	0.4	40	3	US-08-439-996-4	Sequence 4, Appl	361	18	0.4	20	3	US-09-128-496-59	Sequence 59, Appl
c 289	18.4	0.4	40	4	US-09-306-290-36	Sequence 36, Appl	362	18	0.4	20	4	US-09-009-490A-59	Sequence 59, Appl
c 290	18.4	0.4	40	4	US-09-732-067-7	Sequence 7, Appl	c 363	18	0.4	20	4	US-09-082-649B-60	Sequence 60, Appl
c 291	18.2	0.4	27	5	PCT-US92-10792-45	Sequence 45, Appl	364	18	0.4	20	5	PCT-US93-08101-59	Sequence 59, Appl
c 292	18.2	0.4	26	3	US-09-009-913-103	Sequence 103, App	c 365	18	0.4	25	1	US-08-182-619-13	Sequence 13, Appl
c 293	18.2	0.4	31	1	US-08-145-704-9	Sequence 9, Appl	c 366	18	0.4	25	1	US-08-390-858B-13	Sequence 13, Appl
c 294	18.2	0.4	31	3	US-08-987-574-9	Sequence 9, Appl	c 367	18	0.4	25	1	US-08-330-535A-13	Sequence 13, Appl
c 295	18.2	0.4	31	4	US-08-535-168-9	Sequence 9, Appl	c 368	18	0.4	25	2	US-08-838-844-13	Sequence 13, Appl
c 296	18.2	0.4	31	4	US-09-017-974-9	Sequence 9, Appl	c 369	18	0.4	26	1	US-08-487-141B-42	Sequence 42, Appl
c 297	18.2	0.4	31	4	US-08-682-255A-9	Sequence 9, Appl	c 370	18	0.4	26	1	US-08-937-561-42	Sequence 42, Appl
c 298	18.2	0.4	31	4	US-09-429-130-9	Sequence 9, Appl	c 371	18	0.4	26	5	PCT-US96-09388-42	Sequence 42, Appl
c 299	18.2	0.4	31	5	PCT-US96-11786-9	Sequence 9, Appl	372	18	0.4	30	1	US-08-504-511A-6	Sequence 6, Appl
c 300	18.2	0.4	32	5	PCT-US96-08142-4	Sequence 4, Appl	373	18	0.4	30	1	US-08-467-126-6	Sequence 6, Appl
c 301	18.2	0.4	33	3	US-09-061-026-26	Sequence 26, App	374	18	0.4	30	2	US-08-629-001A-44	Sequence 44, Appl
c 302	18.2	0.4	33	3	US-09-466-138-26	Sequence 26, App	375	18	0.4	30	2	US-08-476-712-5	Sequence 5, Appl
c 303	18.2	0.4	34	2	US-08-435-149-24	Sequence 24, App	376	18	0.4	30	4	US-08-642-274D-123	Sequence 123, App
c 304	18.2	0.4	36	2	US-08-596-387B-112	Sequence 112, App	377	18	0.4	31	4	US-09-411-291-5	Sequence 5, Appl
c 305	18.2	0.4	36	4	US-09-067-615-112	Sequence 112, App	378	18	0.4	31	4	US-09-268-505B-13	Sequence 13, Appl
c 306	18.2	0.4	36	5	PCT-US95-09816A-112	Sequence 112, App	c 379	18	0.4	35	1	US-07-844-297-2	Sequence 2, Appl
c 307	18.2	0.4	38	1	US-08-399-696-6	Sequence 6, Appl	380	18	0.4	35	1	US-08-435-350-118	Sequence 118, App
c 308	18.2	0.4	38	2	US-08-467-822-16	Sequence 16, Appl	381	18	0.4	36	1	US-08-435-350-3	Sequence 3, Appl
c 309	18.2	0.4	38	4	US-08-432-697-16	Sequence 16, Appl	c 382	18	0.4	37	1	US-07-915-245-1	Sequence 1, Appl
c 310	18.2	0.4	38	4	US-08-466-248-16	Sequence 16, Appl	383	18	0.4	38	1	US-07-906-871-16	Sequence 16, Appl
c 311	18.2	0.4	39	2	US-09-410-903-73	Sequence 73, Appl	c 384	18	0.4	38	1	US-08-145-704-2	Sequence 2, Appl
c 312	18.2	0.4	39	2	US-08-980-071-20	Sequence 20, Appl	c 385	18	0.4	38	1	US-08-145-704-4	Sequence 4, Appl
c 313	18.2	0.4	39	2	US-08-757-536-20	Sequence 20, Appl	c 386	18	0.4	38	3	US-08-987-574-2	Sequence 2, Appl
c 314	18.2	0.4	39	3	US-08-754-490-8	Sequence 8, Appl	c 387	18	0.4	38	3	US-08-987-574-4	Sequence 4, Appl
c 315	18.2	0.4	39	3	US-09-314-093-20	Sequence 20, Appl	c 388	18	0.4	38	4	US-08-535-168-2	Sequence 2, Appl
c 316	18.2	0.4	39	3	US-08-922-505A-8	Sequence 8, Appl	c 389	18	0.4	38	4	US-08-535-168-4	Sequence 4, Appl
c 317	18.2	0.4	39	3	US-09-250-848-20	Sequence 20, Appl	c 390	18	0.4	38	4	US-09-017-974-2	Sequence 2, Appl
c 318	18.2	0.4	39	4	US-09-251-885-20	Sequence 20, Appl	c 391	18	0.4	38	4	US-09-017-974-4	Sequence 4, Appl
c 319	18.2	0.4	39	4	US-09-306-290-40	Sequence 40, Appl	c 392	18	0.4	38	4	US-08-682-255A-2	Sequence 2, Appl

393	18	0.4	38	4	US-08-682-255A-4	Sequence 4, Appli	466	17.6	0.3	27	1	US-08-758-306-28	Sequence 28, Appl
394	18	0.4	38	4	US-09-429-130-2	Sequence 2, Appli	467	17.6	0.3	27	1	US-08-758-306-1008	Sequence 1008, Appl
395	18	0.4	38	4	US-09-429-130-4	Sequence 4, Appli	468	17.6	0.3	29	3	US-08-814-052-40	Sequence 40, Appl
396	18	0.4	38	5	PCT-US93-09202-10	Sequence 10, Appl	469	17.6	0.3	30	1	US-08-296-793-2	Sequence 2, Appli
397	18	0.4	38	5	PCT-US93-08329-11	Sequence 11, Appl	470	17.6	0.3	30	1	US-08-379-452-25	Sequence 25, Appli
398	18	0.4	38	5	PCT-US96-11786-2	Sequence 2, Appli	471	17.6	0.3	30	3	US-09-409-670-25	Sequence 25, Appli
399	18	0.4	38	5	PCT-US96-11786-4	Sequence 4, Appli	472	17.6	0.3	31	4	US-09-254-352B-31	Sequence 31, Appl
400	18	0.4	39	1	US-08-099-868-11	Sequence 11, Appl	473	17.6	0.3	33	1	US-08-061-889-4	Sequence 4, Appli
401	18	0.4	39	1	US-08-099-868-17	Sequence 17, Appl	474	17.6	0.3	33	1	US-08-438-639-60	Sequence 60, Appl
402	18	0.4	39	1	US-08-330-123A-14	Sequence 14, Appl	475	17.6	0.3	33	1	US-07-813-338A-60	Sequence 60, Appl
403	18	0.4	39	2	US-09-057-762-5	Sequence 5, Appli	476	17.6	0.3	33	1	US-08-462-611-4	Sequence 4, Appli
404	18	0.4	39	3	US-08-326-119A-5	Sequence 5, Appli	477	17.6	0.3	33	2	US-08-470-124-70	Sequence 70, Appl
405	18	0.4	39	4	US-09-580-517-14	Sequence 14, Appl	478	17.6	0.3	33	2	US-07-814-220-10	Sequence 10, Appl
406	18	0.4	39	4	US-09-619-103-4	Sequence 4, Appli	479	17.6	0.3	33	2	US-07-814-220-15	Sequence 15, Appl
407	18	0.4	40	2	US-08-425-684-70	Sequence 70, Appl	480	17.6	0.3	33	2	US-07-812-421-15	Sequence 10, Appl
408	18	0.4	40	2	US-08-628-422-35	Sequence 35, Appl	481	17.6	0.3	33	2	US-07-812-421-15	Sequence 10, Appl
409	18	0.4	40	2	US-08-675-502-70	Sequence 70, Appl	482	17.6	0.3	33	3	US-07-812-421-15	Sequence 15, Appl
410	18	0.4	40	3	US-09-117-708-5	Sequence 5, Appli	483	17.6	0.3	33	3	US-08-441-971-136	Sequence 136, Appl
411	18	0.4	40	3	US-09-117-708-6	Sequence 6, Appli	484	17.6	0.3	33	4	US-08-221-653-136	Sequence 136, Appl
412	18	0.4	40	4	US-09-569-572C-12	Sequence 12, Appl	485	17.6	0.3	33	4	US-08-441-970-136	Sequence 136, Appl
413	17.8	0.3	21	1	US-08-136-118-10	Sequence 10, Appl	486	17.6	0.3	33	4	US-08-623-428B-8	Sequence 8, Appli
414	17.8	0.3	21	1	US-08-222-177A-160	Sequence 160, Appl	487	17.6	0.3	33	5	PCT-US93-08329-15	Sequence 15, Appl
415	17.8	0.3	21	2	US-08-529-878B-9	Sequence 9, Appli	488	17.6	0.3	33	5	PCT-US94-05378-4	Sequence 4, Appli
416	17.8	0.3	21	2	US-08-863-639A-55	Sequence 55, Appl	489	17.6	0.3	34	2	US-08-612-840A-9	Sequence 9, Appli
417	17.8	0.3	21	2	US-08-863-639A-67	Sequence 67, Appl	490	17.6	0.3	34	2	US-08-933-821-11	Sequence 11, Appl
418	17.8	0.3	21	2	US-08-863-639A-68	Sequence 68, Appl	491	17.6	0.3	34	3	US-08-960-507-11	Sequence 11, Appl
419	17.8	0.3	21	2	US-08-863-639A-71	Sequence 71, Appl	492	17.6	0.3	34	4	US-09-136-828-11	Sequence 11, Appl
420	17.8	0.3	21	2	US-08-416-214A-11	Sequence 11, Appl	493	17.6	0.3	34	4	US-09-332-928A-11	Sequence 11, Appl
421	17.8	0.3	27	4	US-08-253-396A-140	Sequence 140, Appl	494	17.6	0.3	34	4	US-09-136-801-11	Sequence 11, Appl
422	17.8	0.3	28	1	US-08-390-858B-11	Sequence 11, Appl	495	17.6	0.3	34	4	US-09-332-929-11	Sequence 11, Appl
423	17.8	0.3	30	1	US-08-361-920-76	Sequence 76, Appl	496	17.6	0.3	35	1	US-08-126-594-11	Sequence 11, Appl
424	17.8	0.3	30	1	US-08-479-939-76	Sequence 76, Appl	497	17.6	0.3	35	1	US-08-465-811A-11	Sequence 11, Appl
425	17.8	0.3	30	1	US-08-068-747-4	Sequence 4, Appli	498	17.6	0.3	35	2	US-08-619-542B-11	Sequence 11, Appl
426	17.8	0.3	30	1	US-08-433-505-9	Sequence 9, Appli	499	17.6	0.3	35	2	US-09-159-106-8	Sequence 8, Appli
427	17.8	0.3	30	1	US-08-483-432-76	Sequence 76, Appl	500	17.6	0.3	35	4	US-09-605-785-815	Sequence 815, App
428	17.8	0.3	30	2	US-08-676-378-1	Sequence 1, Appli							
429	17.8	0.3	30	3	US-08-870-730-9	Sequence 9, Appli							
430	17.8	0.3	30	3	US-08-951-923-11	Sequence 11, Appl							
431	17.8	0.3	30	3	US-09-083-123-3	Sequence 3, Appli							
432	17.8	0.3	30	3	US-09-083-123-7	Sequence 7, Appli							
433	17.8	0.3	30	4	US-08-882-649A-10	Sequence 10, Appl							
434	17.8	0.3	30	4	US-08-589-109A-12	Sequence 12, Appl							
435	17.8	0.3	30	4	US-09-648-040-4	Sequence 4, Appli							
436	17.8	0.3	32	3	US-09-368-931-1	Sequence 1, Appli							
437	17.8	0.3	33	1	US-08-270-584A-3	Sequence 3, Appli							
438	17.8	0.3	33	2	US-08-765-192-3	Sequence 3, Appli							
439	17.8	0.3	33	3	US-09-199-793-3	Sequence 3, Appli							
440	17.8	0.3	33	4	US-08-986-049-2	Sequence 2, Appli							
441	17.8	0.3	35	1	US-08-126-594-16	Sequence 16, Appl							
442	17.8	0.3	35	1	US-08-126-594-17	Sequence 17, Appl							
443	17.8	0.3	35	1	US-08-465-811A-16	Sequence 16, Appl							
444	17.8	0.3	35	1	US-08-465-811A-17	Sequence 17, Appl							
445	17.8	0.3	35	2	US-08-619-542B-16	Sequence 16, Appl							
446	17.8	0.3	35	2	US-08-619-542B-17	Sequence 17, Appl							
447	17.8	0.3	36	1	US-08-361-708-15	Sequence 15, Appl							
448	17.8	0.3	36	1	US-08-536-277-15	Sequence 15, Appl							
449	17.8	0.3	38	2	US-08-467-822-17	Sequence 17, Appl							
450	17.8	0.3	38	3	US-08-863-813A-51	Sequence 51, Appl							
451	17.8	0.3	38	4	US-08-432-697-17	Sequence 17, Appl							
452	17.8	0.3	38	4	US-08-466-248-17	Sequence 17, Appl							
453	17.8	0.3	39	3	US-08-213-741-1	Sequence 1, Appli							
454	17.8	0.3	39	4	US-08-890-929-6	Sequence 6, Appli							
455	17.8	0.3	39	4	US-09-316-083-20	Sequence 20, Appl							
456	17.8	0.3	39	4	US-08-522-336-1	Sequence 1, Appli							
457	17.8	0.3	40	2	US-08-628-422-24	Sequence 24, Appl							
458	17.8	0.3	40	4	US-09-306-290-22	Sequence 22, Appl							
459	17.6	0.3	24	1	US-08-014-943A-5	Sequence 5, Appli							
460	17.6	0.3	24	1	US-08-486-421-4	Sequence 44, Appl							
461	17.6	0.3	24	1	US-08-470-911-44	Sequence 44, Appl							
462	17.6	0.3	24	2	US-08-486-809-44	Sequence 44, Appl							
463	17.6	0.3	24	2	US-08-682-787-71	Sequence 71, Appl							
464	17.6	0.3	24	4	US-09-097-199-71	Sequence 71, Appl							
465	17.6	0.3	24	4	US-09-043-303-16	Sequence 16, Appl							

ALIGNMENTS

RESULT 1

US-07-936-421-2

Sequence 2, Application US/07936421

Patent No. 5750390

GENERAL INFORMATION:

APPLICANT: James D. Thompson

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT OF DISEASES CAUSED BY EXPRESSION OF THE BCL-2

TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2

TITLE OF INVENTION: GENE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/936,421

FILING DATE: 19920826

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: FILING DATE:

none

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 197/243  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-936-421-2

Query Match 0.7%; Score 37; DB 1; Length 37;  
Best Local Similarity 70.3%; Pred. No. 2.6;  
Matches 26; Conservative 11; Mismatches 0; Indels 0; Gaps 0;  
QY 1415 GCGGAGGTGCGTGGCCCGCGTGTGCTTTCCTCT 1451  
1 GCGGAGGCGGCGGUGGCCCGGUGGCUUUUCUCU 37

RESULT 2  
US-07-936-421-15  
; Sequence 15, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
; BY EXPRESSION OF THE BCL-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/936,421  
; FILING DATE: 19920826  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 197/243  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-936-421-15

Query Match 0.7%; Score 36; DB 1; Length 36;  
Best Local Similarity 86.1%; Pred. No. 4.5;  
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 1997 ACCTGAACCGGCACCTGCACACCTGCATCCAGGATA 2032  
1 ACCUGAACCGGCACCGCAGCACCUGGAGGAGGAGGAGG 36

RESULT 3  
US-08-217-082A-2  
; Sequence 2, Application US/08217082A  
; Patent No. 5734033  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE  
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; P.C.  
; STREET: 224 Airport Parkway  
; CITY: San Jose  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 95110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/217,082A  
; FILING DATE: 24-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/840,716  
; FILING DATE: 21-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/288,692  
; FILING DATE: 22-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fortney, Andrew D.  
; REGISTRATION NUMBER: 34,600  
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (408) 436-2070  
; TELEFAX: (408) 436-2075  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: NO  
; US-08-217-082A-2  
Query Match 0.7%; Score 35; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1442 CTTTCTCTCTGGAGGATGGCGCGCTGGGAGA 1476  
1 CTTTCTCTCTGGAGGATGGCGCGCTGGGAGA 35

RESULT 4  
US-07-936-421-20  
; Sequence 20, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:





; FILING DATE: 21-FEB-1992  
; PRIOR APPLICATION DATA: US 07/288,692  
; APPLICATION NUMBER: 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; FILING DATE: 22-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fortney, Andrew D.  
; REGISTRATION NUMBER: 34,600  
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (408) 436-2070  
; TELEFAX: (408) 436-2075  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: NO  
; US-09-080-285-2

Query Match 0.7%; Score 35; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAGGATGCGCAGCTGGGAGA 1476  
|||||  
Db 1 CTTTTCCTCTGGGAGGATGCGCAGCTGGGAGA 35

RESULT 7  
US-09-724-426-2  
; Sequence 2, Application US/09724426  
; Patent No. 6414134  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
; FILE REFERENCE: 10412-024  
; CURRENT APPLICATION NUMBER: US/09/724,426  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-724-426-2

Query Match 0.7%; Score 35; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 CTTTTCCTCTGGGAGGATGCGCAGCTGGGAGA 1476  
|||||  
Db 1 CTTTTCCTCTGGGAGGATGCGCAGCTGGGAGA 35

RESULT 8  
US-07-936-421-16  
; Sequence 16, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2  
; TITLE OF INVENTION: GENE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles

; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/936,421  
; FILING DATE: 19920826  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; APPLICATION NUMBER: described below:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 197/243  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-936-421-16

Query Match 0.7%; Score 34; DB 1; Length 34;  
Best Local Similarity 76.5%; Pred. No. 14;  
Matches 26; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 2043 GGATGCCCTTTGTGGAACGTACGCCGCCAGCATG 2076  
|||||  
Db 1 GGAUGCCUUUGGAAACUGACGCCGCCAGCAUG 34

RESULT 9  
US-07-936-421-21  
; Sequence 21, Application US/07936421  
; Patent No. 5750390  
; GENERAL INFORMATION:  
; APPLICANT: James D. Thompson  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED  
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2  
; TITLE OF INVENTION: GENE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/936,421  
; FILING DATE: 19920826  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; APPLICATION DATA: described below:  
; none

**RESULT 12**

```

; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,784
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/00852
; FILING DATE: 02-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL M195 A 000420
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, John C.
; REGISTRATION NUMBER: 30,413
; REFERENCE/DOCKET NUMBER: 05999.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-894-784-19

Query Match 0.6%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4256 GACCTGTTTCTTGAGGTTTCTCGTCC 4285
      |||||
Db 1 GACCTGTTTCTTGAGGTTTCTCGTCC 30

RESULT 14
US-08-894-784-23
; Sequence 23, Application US/08894784
; Patent No. 6005095
; GENERAL INFORMATION:
; APPLICANT: Capaccioli, Sergio
; APPLICANT: Morelli, Susanna
; APPLICANT: Nicolin, Angelo
; TITLE OF INVENTION: ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR
; TITLE OF INVENTION: CELLS HAVING A T(14;18) TRANSLOCATION AND
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF SAID TUMOR CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,784
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/00852
; FILING DATE: 02-MAR-1996
; CURRENT APPLICATION DATA:

```

```
; APPLICATION NUMBER: IL M195 A 000420
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, John C.
; REGISTRATION NUMBER: 30,413
; REFERENCE/DOCKET NUMBER: 05999.0005-000000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-894-784-23
; Query Match 0.6%; Score 30; DB 3; Length 30;
; Best Local Similarity 100.0%; Pred. No. 1.3e+02;
; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4256 GACCTTCTTCTTCAAGTTTCCTCGGCC 4285
Db 1 GACCTTCTTCTTCAAGTTTCCTCGGCC 30

RESULT 15
US-07-936-421-8
; Sequence 8, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936.421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
US-07-936-421-8
; Query Match 0.6%; Score 28; DB 1; Length 28;
; Best Local Similarity 82.1%; Pred. No. 3.9e+02;
; Matches 23; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1729 CTTGTGTTCACCTGGCCCTCCGCCAAG 1756
Db 1 CCUGUGUCCACCGGCCUCCGCCAAG 28

RESULT 16
US-08-894-784-20/c
; Sequence 20, Application US/08894784
; Patent No. 6005095
; GENERAL INFORMATION:
; APPLICANT: Capaccioli, Sergio
; APPLICANT: Morelli, Susanna
; APPLICANT: Nicolin, Angelo
; TITLE OF INVENTION: ANTISENSE TRANSCRIPT ASSOCIATED TO TUMOR
; TITLE OF INVENTION: CELLS HAVING A T(14;18) TRANSLOCATION AND
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES USEFUL IN THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF SAID TUMOR CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,784
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/00852
; FILING DATE: 02-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL M195 A 000420
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, John C.
; REGISTRATION NUMBER: 30,413
; REFERENCE/DOCKET NUMBER: 05999.0005-000000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-894-784-20
; Query Match 0.6%; Score 28; DB 3; Length 30;
; Best Local Similarity 100.0%; Pred. No. 4e+02;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4504 CTTCAAGGTTCTTCTGAAATGCAGTGGT 4531
Db 30 CTTCAAGGTTCTTCTGAAATGCAGTGGT 3

RESULT 17
```











```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mfd58rs
US-08-222-177A-218

```

Query Match 0.5%; Score 26.8; DB 1; Length 33;

QY	2310	CACACACAGACAGACACACACACACA	2339
Db	1	CACACACACACACACACACACACACA	30

RESULT 28  
US-08-222-177A-110  
; Sequence 110, Application US/08222177A  
; Patent No. 5582979  
; GENERAL INFORMATION:  
; APPLICANT: Weber, James L.  
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
; TITLE OF INVENTION: (gc-da)n.(dg-dt)n SEQUENCES 1  
; NUMBER OF SEQUENCES: 460  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dewitt Ross & Stevens, S.C.  
; STREET: 8000 Excelsior Drive, Suite 401  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: USA  
; ZIP: 53717-1914  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222.177A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/341,562  
; FILING DATE: 21-APR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sara, Charles S.  
; REGISTRATION NUMBER: 30,492  
; REFERENCE/DOCKET NUMBER: 09865.601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 831-2100  
; TELEFAX: (608) 831-2106  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd20rs
US-08-222-177A-110

```

Query Match 0.5%; Score 26.8; DB 1; Length 34;  
Best Local Similarity 93.3%; Pred. No. 8.7e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels

Qy	2310	CACACACACAGACACACACACACA	2339
Db	2	CACACACACACACACACACACACACA	31

```

RESULT 29
US-08-222-177A-172
; Sequence 172, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd41rs
; US-08-222-177A-172

```

Query Match 0.5%; Score 26.8; DB 1; Length 34;  
Best Local Similarity 93.3%; Pred. No. 8.7e+02;  
Matches 28: Conservative 0; Mismatches 2; Indels

QY 2310 CACACACAGACAGACACACACACA 2339  
 ||||| ||| |||||  
 Db 2 CACACACACACACACACACACACACA 31







US-08-222-177A-140

Query Match 0.5%; Score 26.8; DB 1; Length 37;  
Best Local Similarity 93.3%; Pred. No. 9.1e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACA 2339

Db 2 CACACACACACACACACACACACACACA 31

RESULT 38

US-08-222-177A-68

; Sequence 68, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.

; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

; NUMBER OF SEQUENCES: 460

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dewitt Ross &amp; Stevens, S.C.

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: USA

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,177A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/341,562

; FILING DATE: 21-APR-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Sara, Charles S.

; REGISTRATION NUMBER: 30,492

; REFERENCE/DOCKET NUMBER: 09865.601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; TELEX:

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; IMMEDIATE SOURCE:

; CLONE: mfd6irs

US-08-222-177A-68

Query Match 0.5%; Score 26.8; DB 1; Length 38;

Best Local Similarity 93.3%; Pred. No. 9.3e+02;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACA 2339

Db 1 CACACACACACACACACACACACACACA 30

RESULT 39

US-08-222-177A-198

; Sequence 198, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.

; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
; TITLE OF INVENTION: (gc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 460  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dewitt Ross &amp; Stevens, S.C.

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: USA

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,177A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/341,562

; FILING DATE: 21-APR-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Sara, Charles S.

; REGISTRATION NUMBER: 30,492

; REFERENCE/DOCKET NUMBER: 09865.601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; TELEX:

; INFORMATION FOR SEQ ID NO: 198:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; IMMEDIATE SOURCE:

; CLONE: mfd50rs

US-08-222-177A-198

Query Match

Best Local Similarity 93.3%; Pred. No. 9.3e+02;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACA 2339

Db 1 CACACACACACACACACACACACACA 30

RESULT 40

US-08-222-177A-397

; Sequence 397, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.

; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

; NUMBER OF SEQUENCES: 460

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dewitt Ross &amp; Stevens, S.C.

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: USA

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,177A

```

; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd12rs
US-08-222-177A-86

Query Match
Best Local Similarity 0.5%; Score 26.8; DB 1; Length 39;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACAGACACACACACACACA 2339
Db 8 CACACACACACATACACACACACACA 37

RESULT 42
US-08-222-177A-137
; Sequence 137, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd29rs
US-08-222-177A-137

Query Match
Best Local Similarity 0.5%; Score 26.8; DB 1; Length 39;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACAGACACACACACACACA 2339
Db 2 CACACACACACACACACACACACACA 31

RESULT 43
US-08-222-177A-119
; Sequence 119, Application US/08222177A

```



;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; IMMEDIATE SOURCE:  
;; CLONE: mfd34rs  
US-08-222-177A-152

Query Match 0.5%; Score 26.2; DB 1; Length 40;  
Best Local Similarity 79.5%; Pred. No. 1.3e+03;  
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACAAATTAACA 2349  
||||| ||| ||||||||| |||  
Db 1 ACACACACACACACACACACACACACACACACACACAC 39

## RESULT 46

US-08-455-627-25  
Sequence 25, Application US/08455627  
Patent No. 5571677  
;; GENERAL INFORMATION:  
;; APPLICANT: Sergei M. Gryaznov  
;; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply  
;; TITLE OF INVENTION: Connected Macromolecular Structures  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cooley Godward LLP  
;; STREET: Five Palo Alto Square, 3000 El Camino Real  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94306-2155

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/455,627  
;; FILING DATE: 31-MAY-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Nakamura, Jackie N.  
;; REGISTRATION NUMBER: 35,966  
;; REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-843-5000  
;; TELEFAX: 415-857-0663  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 29 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-455-627-25

Query Match 0.5%; Score 25.8; DB 1; Length 29;  
Best Local Similarity 93.1%; Pred. No. 1.4e+03;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACAC 2338  
||||| ||| ||||||||| |||  
Db 1 CACACACACACACACACACACACACAC 29

## RESULT 47

US-08-222-177A-80  
Sequence 80, Application US/08222177A  
Patent No. 5582979  
;; GENERAL INFORMATION:  
;; APPLICANT: Weber, James L.

;; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
;; TITLE OF INVENTION: (GC-DA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME  
;; NUMBER OF SEQUENCES: 460  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dewitt Ross & Stevens, S.C.  
;; STREET: 8000 Excelsior Drive, Suite 401  
;; CITY: Madison  
;; STATE: Wisconsin  
;; COUNTRY: USA  
;; ZIP: 53717-1914  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/222,177A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/341,562  
;; FILING DATE: 21-APR-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sara, Charles S.  
;; REGISTRATION NUMBER: 30,492  
;; REFERENCE/DOCKET NUMBER: 09865.601  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (608) 831-2100  
;; TELEFAX: (608) 831-2106  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 80:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 29 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; IMMEDIATE SOURCE:  
;; CLONE: mfd10rs  
US-08-222-177A-80

Query Match 0.5%; Score 25.8; DB 1; Length 29;  
Best Local Similarity 93.1%; Pred. No. 1.4e+03;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACAC 2339  
||||| ||| ||||||||| |||  
Db 1 ACACACACACACACACACACACACAC 29

## RESULT 48

US-08-222-177A-238  
Sequence 238, Application US/08222177A  
Patent No. 5582979  
;; GENERAL INFORMATION:  
;; APPLICANT: Weber, James L.  
;; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
;; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME  
;; NUMBER OF SEQUENCES: 460  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dewitt Ross & Stevens, S.C.  
;; STREET: 8000 Excelsior Drive, Suite 401  
;; CITY: Madison  
;; STATE: Wisconsin  
;; COUNTRY: USA  
;; ZIP: 53717-1914  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/222,177A



```
;
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd65rs
; US-08-222-177A-238
;
; Query Match 0.5%; Score 25.8; DB 1; Length 29;
; Best Local Similarity 93.1%; Pred. No. 1.4e+03;
; Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2310 CACACACACACACACACACACACAC 2338
; Db 1 CACACACACACACACACACACACAC 29
;
; RESULT 49
; US-08-689-856-25
; Sequence 25, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; QY 2310 CACACACACACACACACACACACAC 2338
; Db 1 CACACACACACACACACACACACAC 29
;
; RESULT 50
; US-08-222-177A-373
; Sequence 373, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-da)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd118rs
; US-08-222-177A-373
;
; Query Match 0.5%; Score 25.8; DB 1; Length 30;
; Best Local Similarity 93.1%; Pred. No. 1.4e+03;
; Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2311 ACACACACACACACACACACACAC 2339
; Db 1 ACACACACACACACACACACACAC 29
;
; Search completed: May 31, 2003, 22:25:54
; Job time : 272 secs
```





C 80	A2826855	2M0102F23	153	23.8	0.5	32	17	A2335085	AZ335085	1M0064F17
C 81	A2837376	2M0132C10	C 154	23.8	0.5	33	17	A2473611	AZ473611	1M0289001
C 82	A2319970	1M0039K17	C 155	23.8	0.5	36	17	A2623245	AZ623245	1M0450C15
C 83	A2338857	1M0070A08	C 156	23.8	0.5	36	17	A2774711	AZ774711	2M0004I17
C 84	A2587825	1M0395F16	C 157	23.8	0.5	31	17	A2822976	AZ822976	2M0096008
C 85	A2603138	1M0422G15	C 158	23.6	0.5	38	17	A2399554	AZ399554	1M0165019
C 86	A2808181	2M0071A18	C 159	23.6	0.5	31	17	A2432709	AZ432709	1M0218C16
C 87	A2819018	2M0089I19	C 160	23.6	0.5	33	17	A2514079	AZ514079	1M0360F07
C 88	A2438581	1M0228D16	C 161	23.6	0.5	34	17	A2483866	AZ483866	1M0310N01
C 89	A2983391	2M0264I05	C 162	23.6	0.5	34	17	A2622092	AZ622092	1M0455H07
C 90	A2513013	1M0358M21	C 163	23.6	0.5	34	17	A2875700	AZ875700	2M0190D19
C 91	A2628646	1M0467E06	C 164	23.6	0.5	35	17	A2580498	AZ580498	1M0368I15
C 92	A2489673	1M0322E18	C 165	23.6	0.5	35	17	A2960947	AZ960947	2M0229M11
C 93	A2480184	1M0301E04	C 166	23.6	0.5	38	17	A2426925	AZ426925	1M0208E11
C 94	A2781595	2M0021P06	C 167	23.6	0.5	39	17	A2588176	AZ588176	1M0396M11
C 95	A2315179	1M0032K18	C 168	23.4	0.5	38	17	A2424085	AZ424085	1M0203B05
C 96	A2414401	1M0188M13	C 169	23.2	0.5	37	17	A2420346	AZ420346	1M0198G12
C 97	A2458713	1M0263L02	C 170	23.2	0.5	37	17	A2484142	AZ484142	1M0310E24
C 98	A2497897	1M0334K20	C 171	23	0.5	33	17	A2345522	AZ345522	1M0080L05
C 99	A2989744	2M0273N10	C 172	23	0.5	36	17	A2982742	AZ982742	2M0263H11
C 100	A2628068	1M0476P22	C 173	23	0.5	39	17	A2826077	AZ826077	2M0101A07
C 101	A2483942	1M0309H20	C 174	23	0.5	40	17	A2479725	AZ479725	1M0300O02
C 102	A2456482	1M0259P11	C 175	23	0.5	40	17	A2800091	AZ800091	2M0057K22
C 103	A2456482	1M0259P11	C 176	22.8	0.4	26	17	A2307889	AZ307889	1M0010L18
C 104	A2837355	2M0162M19	C 177	22.8	0.4	26	17	A2345505	AZ345505	1M0080H01
C 105	A2328984	1M0053H01	C 178	22.8	0.4	26	17	A2494537	AZ494537	1M0329D24
C 106	A2635862	1M0493C04	C 179	22.8	0.4	26	17	A2503652	AZ503652	1M0343F01
C 107	A2459684	1M0537C17	C 180	22.8	0.4	26	17	A2795803	AZ795803	2M0051P11
C 108	A2496969	1M0333E07	C 181	22.8	0.4	26	17	A2806004	AZ806004	2M0067H16
C 109	A2661921	1M0540B17	C 182	22.8	0.4	26	17	A2975568	AZ975568	2M0250L12
C 110	A2509672	1M0352A18	C 183	22.8	0.4	27	17	A2329433	AZ329433	1M0053K11
C 111	A26313057	1M0441C17	C 184	22.8	0.4	27	17	A2788874	AZ788874	2M0036H16
C 112	A2966276	2M0240K02	C 185	22.8	0.4	29	17	A2801217	AZ801217	2M0059P03
C 113	A2875282	1M0189A20	C 186	22.8	0.4	29	17	A2866837	AZ866837	2M0170T01
C 114	A2974885	2M0249P09	C 187	22.6	0.4	29	17	A2807584	AZ807584	2M0070H04
C 115	A2397262	1M0162I12	C 188	22.6	0.4	29	17	A2860659	AZ860659	2M0166F14
C 116	A2330730	1M0056C11	C 189	22.6	0.4	30	17	A2371116	AZ371116	1M0123J05
C 117	A2443611	1M0238N03	C 190	22.6	0.4	32	17	A2797258	AZ797258	2M0053F22
C 118	A2467078	1M0278C15	C 191	22.6	0.4	35	17	A2477397	AZ477397	1M0296D19
C 119	A2514383	1M0361G05	C 192	22.4	0.4	32	17	A2823699	AZ823699	2M0097G23
C 120	A2644345	1M0508E16	C 193	22.4	0.4	32	17	A2338269	AZ338269	1M0069G17
C 121	A2648665	1M0517J18	C 194	22.4	0.4	32	17	A2886648	AZ886648	2M0149B14
C 122	A2649197	1M0518E11	C 195	22.4	0.4	37	17	A2595102	AZ595102	1M0407F03
C 123	A2777903	2M0012D16	C 196	22.2	0.4	28	17	A2442363	AZ442363	1M0236B17
C 124	A2812746	2M0079H07	C 197	22.2	0.4	28	17	A2640238	AZ640238	1M0502H10
C 125	A2786559	2M0032D12	C 198	22	0.4	30	17	A2625192	AZ625192	1M0464J22
C 126	A2412174	1M0185H01	C 199	22	0.4	33	17	A2643646	AZ643646	1M0507A17
C 127	A2579506	1M0367E06	C 200	22	0.4	37	17	A2931583	AZ931583	1M0071H01
C 128	A2829236	2M0106H16	C 201	22	0.4	38	17	A2829800	AZ829800	2M0107I09
C 129	A2807557	2M0070B06	C 202	22	0.4	39	17	A2590136	AZ590136	1M0399K05
C 130	A2841151	1M0413D04	C 203	22	0.4	39	17	A2643646	AZ643646	1M0507A17
C 131	A2304813	1M0005L18	C 204	22	0.4	40	17	A2628038	AZ628038	1M0476N17
C 132	A1539675	tp71f03.x	C 205	21.8	0.4	25	17	A2339866	AZ339866	1M0071H01
C 133	A2491991	1M0325C24	C 206	21.8	0.4	25	17	A2404057	AZ404057	1M0172D10
C 134	A2511942	1M0357O08	C 207	21.8	0.4	25	17	A2769673	AZ769673	1M0570D12
C 135	A2512195	1M0357O04	C 208	21.8	0.4	25	17	A2771881	AZ771881	1M0574F23
C 136	A2663681	1M0543M21	C 209	21.8	0.4	26	17	A2419877	AZ419877	1M0196N03
C 137	A2774254	2M0003L23	C 210	21.8	0.4	26	17	A2646850	AZ646850	1M0513L06
C 138	A2425112	1M0205I01	C 211	21.8	0.4	26	17	A2830551	AZ830551	2M0109C19
C 139	A2815799	2M0084F24	C 212	21.8	0.4	33	17	A2766046	AZ766046	1M0563N18
C 140	TAVAL12P	T. brucei	C 213	21.8	0.4	33	17	A2799903	AZ799903	2M0057G08
C 141	A2440652	1M0231N14	C 214	21.8	0.4	33	17	A2826970	AZ826970	2M0103C06
C 142	A2494653	1M0330K03	C 215	21.8	0.4	34	17	A2656447	AZ656447	1M0532C02
C 143	A2803691	2M0064A17	C 216	21.8	0.4	38	12	BG778513	BG778513	60266730
C 144	A2342492	1M0075O04	C 217	21.6	0.4	31	17	A2346705	AZ346705	1M0082M02
C 145	A2435344	1M0322K17	C 218	21.6	0.4	37	17	A2666510	AZ666510	1M0548M11
C 146	A2583081	1M0376L16	C 219	21.6	0.4	38	17	A2490125	AZ490125	1M0322J19
C 147	A2638238	1M0498H05	C 220	21.6	0.4	38	17	AZ500372	AZ500372	1M0338M11
C 148	A2758321	1M0550G18	C 221	21.6	0.4	40	17	AZ465284	AZ465284	1M0275B10
C 149	A2981811	2M0262D23	C 222	21.4	0.4	31	17	AZ781134	AZ781134	2M0019B09
C 150	A2366137	1M0115B21	C 223	21.4	0.4	34	17	AZ814562	AZ814562	2M0082A22
C 151	A2405219	1M0173N21	C 224	21.4	0.4	37	17	AZ784558	AZ784558	2M0027G15
C 152	AZ782113	2M0022N03	C 225	21.4	0.4	38	9	AU266086	AU266086	

226	21.4	0.4	39	17	AZ861762	AZ861762	2M0168J10	C 299	20.4	0.4	38	17	AZ861891	AZ861891	2M0168H15
227	21.4	0.4	39	17	AZ949919	AZ949919	2M0213B16	300	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
228	21.4	0.4	39	17	AL764506	AL764506	Arabidops	301	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
229	21.4	0.4	39	17	AL764506	AL764506	Arabidops	302	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
230	21.4	0.4	39	17	AL764506	AL764506	Arabidops	303	20.4	0.4	38	17	AZ863994	AZ863994	2M0173B22
231	21.4	0.4	40	17	AL198940	AL198940	qf66f09.x	C 303	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
232	21.4	0.4	40	17	AZ369493	AZ369493	1M0120B11	304	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
233	21.4	0.4	40	17	AZ879767	AZ879767	2M0037D20	305	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
234	21.2	0.4	26	17	AZ494629	AZ494629	1M0330F01	306	20.4	0.4	39	17	AZ863994	AZ863994	2M0173B22
235	21.2	0.4	26	17	AZ766495	AZ766495	1M0564D08	C 307	20.4	0.4	9	AA452094	AA452094	zx30h08.s	
236	21.2	0.4	26	17	AZ781130	AZ781130	2M0019A07	C 308	20.4	0.4	40	14	D21037	D21037	HUMGS02020
237	21.2	0.4	26	17	AZ646963	AZ646963	1M0513C13	309	20.2	0.4	25	17	AZ451588	AZ451588	1M0231I05
238	21.2	0.4	27	17	AZ946507	AZ946507	2M0208O18	310	20.2	0.4	25	17	AZ780500	AZ780500	2M0017J19
239	21.2	0.4	33	17	TA34G07P	TA34G07P	T. brucei	C 311	20.2	0.4	26	17	AZ467063	AZ467063	1M0278O07
240	21.2	0.4	34	17	AZ322675	AZ322675	1M043D10	C 312	20.2	0.4	33	12	BE86705	BE86705	601507961
241	21.2	0.4	34	17	AZ771845	AZ771845	1M0574M14	C 313	20.2	0.4	33	17	AZ373632	AZ373632	1M0126B22
242	21.2	0.4	40	12	BF213125	BF213125	601844961	C 314	20.2	0.4	33	17	AZ627977	AZ627977	1M0476L03
243	21.2	0.4	40	12	BF213125	BF213125	601844961	C 315	20.2	0.4	34	10	AV857665	AV857665	AV857665
244	21	0.4	30	17	AZ809317	AZ809317	2M0073F14	C 316	20.2	0.4	34	17	AZ514577	AZ514577	1M03361P11
245	21	0.4	36	9	AL639933	AL639933	AL639933	C 317	20.2	0.4	34	17	AZ645914	AZ645914	1M0511K08
246	21	0.4	37	17	AZ654776	AZ654776	1M0529M10	C 318	20.2	0.4	35	17	AZ838204	AZ838204	2M0133K17
247	21	0.4	38	17	AZ402445	AZ402445	1M0169D13	319	20.2	0.4	36	17	AZ766476	AZ766476	1M0269M12
248	21	0.4	38	17	AZ655948	AZ655948	1M0531N12	C 320	20.2	0.4	36	17	AZ766476	AZ766476	1M0269M12
249	21	0.4	38	17	AZ949765	AZ949765	2M0213D06	C 321	20.2	0.4	36	17	AL763948	AL763948	Arabidops
250	21	0.4	39	17	BH789389	BH789389	SALK_0191	C 322	20.2	0.4	37	17	AZ498469	AZ498469	1M0335I17
251	21	0.4	39	17	AL757684	AL757684	Arabidops	323	20.2	0.4	37	17	TA51G08Q	TA51G08Q	T. brucei
252	21	0.4	40	2	HSM002456	AL038117	Homo sapi	324	20.2	0.4	40	10	AW248768	AW248768	2820919.3
253	21	0.4	40	17	TA115808P	AL462822	T. brucei	325	20.2	0.4	9	HSM003149	HSM003149	Homo sapi	
254	20.8	0.4	24	17	AZ419602	AZ419602	1M0196L12	326	20.2	0.4	40	9	AI697142	AI697142	1M0511K08
255	20.8	0.4	24	17	AZ446429	AZ446429	1M0242A24	C 327	20	0.4	29	14	N53413	N53413	2M0173B22
256	20.8	0.4	24	17	AZ621455	AZ621455	1M0454K11	C 328	20	0.4	29	17	AZ826631	AZ826631	2M0102E22
257	20.8	0.4	24	17	AZ807762	AZ807762	2M0070014	C 329	20	0.4	31	17	TA338C10P	TA338C10P	T. brucei
258	20.8	0.4	24	17	AZ813106	AZ813106	2M0080A16	C 330	20	0.4	34	17	AZ475648	AZ475648	1M0293G05
259	20.8	0.4	24	17	AZ846178	AZ846178	2M0146F14	C 331	20	0.4	34	17	AZ990901	AZ990901	2M0274N14
260	20.8	0.4	24	17	TA163H11P	AL472248	T. brucei	C 332	20	0.4	36	17	AZ337595	AZ337595	1M0068O17
261	20.8	0.4	25	17	AZ345553	AZ345553	1M0080E16	333	20	0.4	36	17	AZ623038	AZ623038	1M0460L13
262	20.8	0.4	25	17	AZ465273	AZ465273	1M0275P01	334	20	0.4	36	17	AZ623038	AZ623038	1M0460L13
263	20.8	0.4	25	17	AZ467470	AZ467470	1M0278E21	335	20	0.4	36	17	AZ623038	AZ623038	1M0460L13
264	20.8	0.4	25	17	AZ762101	AZ762101	1M0556K17	336	20	0.4	36	17	AZ643259	AZ643259	1M0506G06
265	20.8	0.4	33	17	TA245A09Q	AL482142	T. brucei	337	20	0.4	36	17	AZ772448	AZ772448	1M0583O18
266	20.8	0.4	33	17	TA356C09P	AL497114	T. brucei	C 338	20	0.4	36	17	AZ777975	AZ777975	2M0010I18
267	20.8	0.4	34	9	AI122781	AI122781	q848g10.x	339	20	0.4	36	17	AZ779933	AZ779933	2M0056D07
268	20.8	0.4	34	10	AW251037	AW251037	2821413.3	340	20	0.4	36	17	AZ806045	AZ806045	2M0067P17
269	20.8	0.4	35	17	AZ639148	AZ639148	1M0499M21	341	20	0.4	36	17	AZ806045	AZ806045	2M0067P17
270	20.8	0.4	35	17	AZ663471	AZ663471	1M0543D09	342	20	0.4	36	17	AZ829267	AZ829267	2M0106O14
271	20.8	0.4	37	9	AA873697	AA873697	ob36g11.s	343	20	0.4	36	17	AZ847638	AZ847638	2M0148K14
272	20.8	0.4	40	17	AZ330731	AZ330731	1M0056C12	C 344	20	0.4	37	9	AA903696	AA903696	ok54h06.s
273	20.8	0.4	40	17	AZ556548	AZ556548	1M0532H11	345	20	0.4	37	9	AI129902	AI129902	qc41b07.x
274	20.8	0.4	40	17	AZ761020	AZ761020	1M0555E08	346	20	0.4	37	9	AA118459	AA118459	zv92h04.r
275	20.8	0.4	40	17	AZ813980	AZ813980	2M0081D06	C 347	20	0.4	37	17	AZ311322	AZ311322	1M0026N11
276	20.8	0.4	40	17	AZ952893	AZ952893	2M0217G24	348	20	0.4	37	17	AZ459123	AZ459123	1M0263D16
277	20.6	0.4	28	9	AU264164	AU264164	AU264164	349	20	0.4	37	17	AZ761163	AZ761163	1M0555P18
278	20.6	0.4	28	17	AZ345426	AZ345426	1M0080A09	350	20	0.4	37	17	AZ771220	AZ771220	1M0573A15
279	20.6	0.4	28	17	AZ466703	AZ466703	1M0277N06	351	20	0.4	37	17	AZ853189	AZ853189	2M0156D13
280	20.6	0.4	31	14	RI4943	RI4943	Yf94g04.rl	352	20	0.4	37	17	AZ997433	AZ997433	2M0284A01
281	20.6	0.4	35	17	AZ317100	AZ317100	1M0035E01	353	20	0.4	37	17	TA226A08Q	TA226A08Q	T. brucei
282	20.6	0.4	35	17	AZ389253	AZ389253	1M0149K07	354	20	0.4	38	17	AZ589726	AZ589726	1M0398I24
283	20.6	0.4	35	17	AZ581591	AZ581591	1M0370O23	355	20	0.4	38	17	AZ589726	AZ589726	1M0398I24
284	20.6	0.4	35	17	AZ588848	AZ588848	1M0397M24	C 356	20	0.4	39	17	AZ657455	AZ657455	1M0533H08
285	20.6	0.4	36	17	AZ764529	AZ764529	1M0560L17	C 357	20	0.4	39	9	AL636986	AL636986	AL636986
286	20.6	0.4	36	17	TA270H08P	AL484129	T. brucei	C 358	20	0.4	39	9	AU265743	AU265743	AU265743
287	20.6	0.4	37	17	AZ369295	AZ369295	1M0119M13	C 359	20	0.4	39	9	AU270022	AU270022	AU270022
288	20.4	0.4	37	10	BE539470	BE539470	601060134	360	20	0.4	39	13	BI694035	BI694035	603342221
289	20.4	0.4	31	17	AZ402199	AZ402199	1M0169H20	361	20	0.4	39	17	CNS004NT	CNS004NT	603342221
290	20.4	0.4	31	17	AZ775768	AZ775768	2M0008F23	C 362	20	0.4	39	17	TA116F09P	TA116F09P	AL054298
291	20.4	0.4	34	17	AZ774656	AZ774656	2M0004K10	C 363	20	0.4	39	17	TA200E07Q	TA200E07Q	AL054298
292	20.4	0.4	35	9	AL787430	AL787430	AL787430	364	20	0.4	40	2	HSM002701	HSM002701	AL054298
293	20.4	0.4	37	17	AZ340720	AZ340720	1M0072022	C 365	20	0.4	40	13	BG976639	BG976639	602846941
294	20.4	0.4	38	10	AW332997	AW332997	S16A3 AGS	C 366	19.8	0.4	40	17	AZ466333	AZ466333	1M0276P22
295	20.4	0.4	38	17	AZ462853	AZ462853	1M0271D22	C 367	19.8	0.4	40	17	AZ466333	AZ466333	1M0276P22
296	20.4	0.4	38	17	AZ512402	AZ512402	1M0357H20	C 368	19.8	0.4	23	17	AZ483624	AZ483624	1M0309C01
297	20.4	0.4	38	17	AZ764657	AZ764657	1M0561J11	369	19.8	0.4	23	17	AZ637290	AZ637290	1M0496005
298	20.4	0.4	38	17	AZ777129	AZ777129	2M0011P18	371	19.8	0.4	23	17	AZ828969	AZ828969	2M0106O13

372	19.8	0.4	23	17	AZ829195	AZ829195	2M0106M12	445	19.2	0.4	27	17	AZ827502	AZ827502	2M0103020
c 373	19.8	0.4	24	17	AZ647335	AZ647335	1M0513J15	446	19.2	0.4	30	17	AZ790051	AZ790051	2M0038P15
c 374	19.8	0.4	25	17	AZ766498	AZ766498	1M0564E08	447	19.2	0.4	32	9	AL587570	AL587570	AL587570
c 375	19.8	0.4	31	17	AZ861612	AZ861612	2M0168P16	448	19.2	0.4	32	17	AZ316355	AZ316355	1M0034H10
c 376	19.8	0.4	32	2	HSM003156	HSM003156	AL038680 Homo sapi	c 449	19.2	0.4	32	17	AZ764538	AZ764538	1M0560N21
c 377	19.8	0.4	33	9	AU013658	AU013658	AL038680 Homo sapi	450	19.2	0.4	33	9	AU258912	AU258912	AU258912
c 378	19.8	0.4	34	10	AV674152	AV674152	AV674152 AV674152	451	19.2	0.4	33	9	AU269499	AU269499	AU269499
c 379	19.8	0.4	34	10	AW334249	AW334249	S32D4 AGS	452	19.2	0.4	33	17	AZ404047	AZ404047	1M0172A10
c 380	19.8	0.4	34	17	AZ344610	AZ344610	1M0080C24	453	19.2	0.4	33	17	AZ484644	AZ484644	1M0311H13
c 381	19.8	0.4	35	12	BE894837	BE894837	601434018	454	19.2	0.4	33	17	AZ484644	AZ484644	1M0311H13
c 382	19.8	0.4	35	17	AZ636745	AZ636745	1M0495F14	c 455	19.2	0.4	33	17	AZ620923	AZ620923	1M0453P17
c 383	19.8	0.4	35	17	AZ845779	AZ845779	1M0495F14	c 456	19.2	0.4	33	17	AZ793186	AZ793186	2M0046A13
c 384	19.8	0.4	37	9	AL687908	AL687908	tp89g12.x	c 457	19.2	0.4	33	17	TA95A01P	TA95A01P	AL458992 T. brucei
c 385	19.8	0.4	38	17	TA264B08P	TA264B08P	AL483993 T. brucei	c 458	19.2	0.4	33	12	BG612023	BG612023	602613924
c 386	19.8	0.4	40	9	AU263859	AU263859	AU263859 AU263859	c 459	19.2	0.4	35	17	AZ351309	AZ351309	1M0089K13
c 387	19.8	0.4	40	9	AU264483	AU264483	AU264483 AU264483	c 460	19.2	0.4	36	12	BE894682	BE894682	601435925
c 388	19.8	0.4	40	14	C00202	C00202	HUMS000586	c 461	19.2	0.4	36	17	AZ456524	AZ456524	1M0253I18
c 389	19.8	0.4	40	17	AZ793917	AZ793917	2M0047L24	c 462	19.2	0.4	37	9	AI267817	AI267817	AZ6269612
c 390	19.6	0.4	26	17	AZ774981	AZ774981	2M0004D22	c 463	19.2	0.4	37	13	BJ054011	BJ054011	BJ054011
c 391	19.6	0.4	26	17	TA70E08Q	TA70E08Q	AL458162 T. brucei	c 464	19.2	0.4	37	17	TA15E07P	TA15E07P	AL462838 T. brucei
c 392	19.6	0.4	27	17	AZ404479	AZ404479	1M0172F18	c 465	19.2	0.4	37	17	TA256H06P	TA256H06P	AL482526 T. brucei
c 393	19.6	0.4	27	17	TA287F07P	TA287F07P	AL487522 T. brucei	c 466	19.2	0.4	38	9	AU269612	AU269612	AU269612
c 394	19.6	0.4	31	9	AI364457	AI364457	qw38ell.x	c 467	19.2	0.4	39	9	AU271278	AU271278	AU271278
c 395	19.6	0.4	31	9	AI973247	AI973247	wr53f10.x	c 468	19.2	0.4	39	17	BH789389	BH789389	BH789389
c 396	19.6	0.4	34	10	AW698832	AW698832	r440 non-	c 469	19.2	0.4	39	9	AI424339	AI424339	te95el2.x
c 397	19.6	0.4	35	12	BF338797	BF338797	602036229	c 470	19.2	0.4	40	12	BG772038	BG772038	602721673
c 398	19.6	0.4	35	17	AZ321115	AZ321115	1M0041H02	c 471	19.2	0.4	40	13	BI668945	BI668945	603294924
c 399	19.6	0.4	35	17	BH000551	BH000551	2M0288F03	c 472	19.2	0.4	40	17	AZ335687	AZ335687	1M0065D23
c 400	19.6	0.4	36	13	BI761940	BI761940	603048772	c 473	19.2	0.4	40	17	AZ391073	AZ391073	1M0152I24
c 401	19.6	0.4	36	17	AZ627849	AZ627849	1M0474I13	c 474	19.2	0.4	40	17	BH791898	BH791898	1M0152I24
c 402	19.6	0.4	37	9	AI018534	AI018534	ou24h12.x	c 475	19.2	0.4	40	17	AZ325394	AZ325394	1M0047F17
c 403	19.6	0.4	37	9	AI037939	AI037939	ox53b01.x	c 476	19.2	0.4	28	17	AZ781477	AZ781477	1M0019H24
c 404	19.6	0.4	37	12	BG430173	BG430173	602495159	c 477	19.2	0.4	28	17	AZ961930	AZ961930	2M0230L03
c 405	19.6	0.4	37	12	AZ442522	AZ442522	1M0236D07	c 478	19.2	0.4	30	9	AU266910	AU266910	AU266910
c 406	19.6	0.4	38	12	BF525501	BF525501	602069592	c 479	19.2	0.4	30	17	AZ386218	AZ386218	1M0145M04
c 407	19.6	0.4	38	12	BF526154	BF526154	602071057	c 480	19.2	0.4	32	14	RI6114	RI6114	ya51f03.s2
c 408	19.6	0.4	38	17	AZ484773	AZ484773	1M0311B02	c 481	19.2	0.4	34	9	AL683575	AL683575	tw52b11.x
c 409	19.6	0.4	38	17	AZ776539	AZ776539	2M0010D15	c 482	19.2	0.4	35	9	AL632985	AL632985	AL632985
c 410	19.6	0.4	39	9	AU264049	AU264049	AU264049 AU264049	c 483	19.2	0.4	35	17	AZ609583	AZ609583	1M0434L13
c 411	19.6	0.4	39	12	BG287495	BG287495	602384505	c 484	19.2	0.4	35	17	AZ764499	AZ764499	1M0560K05
c 412	19.6	0.4	40	9	AL804001	AL804001	AL804001 AL804001	c 485	19.2	0.4	35	17	AZ764535	AZ764535	1M0560A22
c 413	19.6	0.4	40	12	BG166502	BG166502	602339795	c 486	19.2	0.4	35	17	AZ784082	AZ784082	2M0028E04
c 414	19.6	0.4	40	17	AZ789792	AZ789792	2M0037J19	c 487	19.2	0.4	35	17	AZ817073	AZ817073	2M0086D07
c 415	19.4	0.4	21	17	AZ626965	AZ626965	1M0467E15	c 488	19.2	0.4	35	17	AZ831930	AZ831930	2M0110E21
c 416	19.4	0.4	27	17	AZ763599	AZ763599	1M0559E08	c 489	19.2	0.4	35	17	AZ858898	AZ858898	2M0164H14
c 417	19.4	0.4	29	17	AZ666737	AZ666737	1M0549Q06	c 490	19.2	0.4	35	17	AZ861607	AZ861607	2M0168P11
c 418	19.4	0.4	29	17	AZ825156	AZ825156	2M0100N08	c 491	19.2	0.4	35	17	AZ967442	AZ967442	2M0238F20
c 419	19.4	0.4	30	17	AZ412824	AZ412824	1M0186F02	c 492	19.2	0.4	35	17	AZ969917	AZ969917	2M0242D20
c 420	19.4	0.4	30	17	AZ486010	AZ486010	1M0313F15	c 493	19.2	0.4	35	17	AL752534	AL752534	Arabiidops
c 421	19.4	0.4	30	17	TA226G05P	TA226G05P	AL480085 T. brucei	c 494	19.2	0.4	36	13	BI078346	BI078346	602874206
c 422	19.4	0.4	31	9	AI677781	AI677781	wc80c06.x	c 495	19.2	0.4	36	17	AZ970687	AZ970687	2M0243I23
c 423	19.4	0.4	31	17	AZ486763	AZ486763	1M0315A11	c 496	19.2	0.4	37	9	AA934710	AA934710	oo72a03.s
c 424	19.4	0.4	31	17	AZ967197	AZ967197	2M0238H01	c 497	19.2	0.4	37	9	AL587823	AL587823	AL587823
c 425	19.4	0.4	32	17	AZ314322	AZ314322	1M0031N05	c 498	19.2	0.4	37	17	AZ623276	AZ623276	1M0460M16
c 426	19.4	0.4	32	17	AZ451231	AZ451231	1M0250I05	c 499	19.2	0.4	38	10	AW333985	AW333985	S28H9 AGS
c 427	19.4	0.4	33	17	AZ586641	AZ586641	1M0392N08	c 500	19.2	0.4	38	17	AL763877	AL763877	Arabiidops
c 428	19.4	0.4	33	17	AZ661578	AZ661578	1M0540C08								
c 429	19.4	0.4	34	17	AZ476549	AZ476549	1M0295P24								
c 430	19.4	0.4	34	17	AZ510095	AZ510095	1M0354B20								
c 431	19.4	0.4	35	9	AL641482	AL641482	AL641482								
c 432	19.4	0.4	35	10	AV966617	AV966617	AV966617								
c 433	19.4	0.4	36	17	AZ328537	AZ328537	1M0052B23								
c 434	19.4	0.4	36	17	TA270G05P	TA270G05P	AL484122 T. brucei								
c 435	19.4	0.4	37	17	AZ758338	AZ758338	1M0550J17								
c 436	19.4	0.4	37	17	DR11K9T	DR11K9T	AL749437 Danio rer								
c 437	19.4	0.4	38	17	AZ600409	AZ600409	1M0418A07								
c 438	19.4	0.4	39	2	HSM002488	HSM002488	AL038149 Homo sapi								
c 439	19.4	0.4	39	14	D25655	D25655	HUMS04003								
c 440	19.4	0.4	40	2	HSM001841	HSM001841	AL037510 Homo sapi								
c 441	19.4	0.4	40	9	AL638703	AL638703	AL638703								
c 442	19.2	0.4	25	17	AZ459694	AZ459694	AZ459694 1M0264P10								
c 443	19.2	0.4	25	17	AZ506209	AZ506209	1M0347F10								
c 444	19.2	0.4	27	17	AZ784556	AZ784556	2M0027E07								

## ALIGNMENTS

RESULT 1  
AZ813889/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ813889  
2M0081B23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
clone UUGC2M0081B23 F, DNA sequence.  
AZ813889  
house mouse.  
GSS.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

39 bp  
DNA  
linear  
GSS 20-FEB-2001

REFERENCE  
AUTHORS

1 (bases 1 to 39)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: B column: 23

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

1. .39

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M081B23"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

5 a 0 c 16 g 18 t

## BASE COUNT

ORIGIN

Query Match

Best Local Similarity 0.6%; Score 31; DB 17; Length 39;

Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACATTAAC 2348

Db 39 CACACACACACACACACACACACACACTTACATTAC 1

## RESULT 2

AZ647581/c

LOCUS

DEFINITION AZ647581 37 bp DNA linear GSS 14-DEC-2000

Clone UUGC1M0514J14 F, DNA sequence.

ACCESSION AZ647581

VERSION AZ647581.1 GI:11779189

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

AUTHORS

1 (bases 1 to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0514 row: J column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

1. .37

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0514J14"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (g14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

0 a 0 c 18 g 19 t

## BASE COUNT

ORIGIN

Query Match

Best Local Similarity 0.6%; Score 29.2; DB 17; Length 37;

Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2343

Db 36 CACACACACACACACACACACACACACACAA 3

## RESULT 3

AZ832583

LOCUS

DEFINITION AZ832583 35 bp DNA linear GSS 20-FEB-2001

clone UUGC2M0113N06 F, DNA sequence.

ACCESSION AZ832583

VERSION AZ832583.1 GI:13002491

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.







REFERENCE  
AUTHORS

1 (bases 1 to 34)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0005 row: A column: 14

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 34.

## FEATURES

Location/Qualifiers

source

1..34  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M005A14"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

Query Match 0.6%; Score 28.2; DB 17; Length 34;  
Best Local Similarity 90.9%; Pred. No. 3.4e+05;  
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2311 ACACACACACACACACACACACACACACAA 2343

||||||| ||| ||||||||||| |||  
Db 34 ACACACACACACACACACACACACACACAA 2

## RESULT 8

AZ803581/c

LOCUS

DEFINITION  
2M0064L05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0064L05 F, DNA sequence.

ACCESSION

AZ803581

VERSION

AZ803581.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 38)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0064 row: L column: 05

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 38.

## FEATURES

Location/Qualifiers

source

1..38  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0064L05"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

Query Match 0.6%; Score 28; DB 17; Length 38;  
Best Local Similarity 86.1%; Pred. No. 3.7e+05;  
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2310 CACACACACACACACACACACACACACAAATT 2345

||||||| ||| ||||||||||| |||  
Db 38 CACACACACACACACACACACACACACAAACT 3

## RESULT 9

AZ638769/c

LOCUS

DEFINITION  
1M0498B20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0498B20 R, DNA sequence.

ACCESSION

AZ638769

VERSION

AZ638769.1

KEYWORDS

GSS.

SOURCE

ORGANISM

house mouse.

Mus musculus

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS      1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0498 row: B column: 20
             Seq primer: CACACAGAAACACTATGACC
             Class: plasmid ends
             High quality sequence stop: 33.
             Location/Qualifiers
FEATURES     source
             1..33
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0498B20"
               /clone.lib="Mouse 10kb plasmid UUGC1M library"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PWD42 (gil14732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
BASE COUNT   0 a    0 c    15 g    18 t
ORIGIN
Query Match          0.5%; Score 27.8; DB 17; Length 33;
Best Local Similarity 93.5%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACAA 2340
||||||| ||| ||||| ||||| ||||| |||||
Db 32 CACACACACACACACACACACACACACAA 2

RESULT 10
AZ365445/c
LOCUS           34 bp DNA linear GSS 02-OCT-2000
DEFINITION      lM0112B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                 clone UUGC1M0112B09 F, DNA sequence.
ACCESSION       AZ365445
VERSION         AZ365445.1 GI:10479145
KEYWORDS        GSS.
SOURCE          house mouse.
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0112 row: B column: 09
             Seq primer: CGTTGTAAACGACGCCAGT
             Class: plasmid ends
             High quality sequence stop: 34.
             Location/Qualifiers
FEATURES     source
             1..34
               /organism="Mus musculus"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0112B09"
               /clone.lib="Mouse 10kb plasmid UUGC1M library"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PWD42 (gil14732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
BASE COUNT   0 a    0 c    16 g    18 t
ORIGIN
Query Match          0.5%; Score 27.8; DB 17; Length 34;
Best Local Similarity 93.5%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACAA 2340
||||||| ||| ||||| ||||| ||||| |||||
Db 31 CACACACACACACACACACACACACACAA 1

RESULT 11
AZ612777/c
LOCUS           35 bp DNA linear GSS 13-DEC-2000
DEFINITION      lM0439P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                 clone UUGC1M0439P13 R, DNA sequence.
ACCESSION       AZ612777
VERSION         AZ612777.1 GI:11734967
KEYWORDS        GSS.
SOURCE          house mouse.
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```



```

REFERENCE
AUTHORS
1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: G column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089G02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      17 g      18 t
ORIGIN
Query Match      0.5%; Score 27.8; DB 17; Length 35;
Best Local Similarity 93.5%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340
|||||
Db 31 CACACACACACACACACACACACACACAA 1

RESULT 14
AZ411170/c
LOCUS
DEFINITION
A411170 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0184D09 F, DNA sequence.
ACCESSION
A411170
VERSION
A411170.1 GI:10535183
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: D column: 09
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0184D09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      1 a      0 c      18 g      17 t
ORIGIN
Query Match      0.5%; Score 27.8; DB 17; Length 36;
Best Local Similarity 93.5%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2309 TCACACACACACACACACACACACACA 2339
|||||
Db 35 TCACACACACACACACACACACACACA 5

RESULT 15
AZ826021/c
LOCUS
DEFINITION
A2826021 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0101F02 R, DNA sequence.
ACCESSION
A2826021
VERSION
A2826021.1 GI:12995929
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE  
AUTHORS

1 (bases 1 to 37)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

JOURNAL  
COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0101 row: F column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

FEATURES  
source

1..37

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0101F02"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 19 t

## ORIGIN

Query Match

Best Local Similarity 0.5%; Score 27.8; DB 17; Length 37;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAA 2340

||||| ||| ||||| ||||| |||||

Db 31 CACACACACACACACACACACACACACAA 1

## RESULT 16

A2346424/c

LOCUS

1M081N12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M081N12 R, DNA sequence.

ACCESSION A2346424

VERSION A2346424.1

GI:10425661

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 39)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

JOURNAL  
COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: N column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

FEATURES  
source

1..39

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M081N12"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 18 g 20 t

## ORIGIN

Query Match

Best Local Similarity 82.1%; Score 27.8; DB 17; Length 39;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAAATTAAAC 2348

||||| ||| ||||| ||||| ||||| |||||

Db 39 CACACACACACACACACACACACACACACACACACACAA 1

## RESULT 17

A2765740/c

LOCUS

1M0562C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0562C19 R, DNA sequence.

ACCESSION A2765740

VERSION A2765740.1

GI:12882075

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```
REFERENCE
AUTHORS
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0562 row: C column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
FEATURES
source
1..39
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0562C19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gll47321l14|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 19 g 20 t
ORIGIN
Query Match 0.5%; Score 27.8; DB 17; Length 39;
Best Local Similarity 93.5%; Pred. No. 4e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Caps 0;
QY 2310 CACACACACACACACACACACACACACAA 2340
||||| ||| ||||| ||||| |||||
Db 31 CACACACACACACACACACACACACACAA 1
RESULT 18
AZ513473/c
LOCUS
DEFINITION
AZ513473 40 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0359021 R, DNA sequence.
ACCESSION
AZ513473
VERSION
AZ513473.1 GI:10694789
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0359 row: O column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
FEATURES
source
1..40
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0359021"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gll47321l14|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 0 a 0 c 19 g 21 t
ORIGIN
Query Match 0.5%; Score 27.8; DB 17; Length 40;
Best Local Similarity 93.5%; Pred. No. 4e+05;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Caps 0;
QY 2310 CACACACACACACACACACACACACACAA 2340
||||| ||| ||||| ||||| |||||
Db 31 CACACACACACACACACACACACACACAA 1
RESULT 19
AZ606329/c
LOCUS
DEFINITION
AZ606329 32 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0428K07 F, DNA sequence.
ACCESSION
AZ606329
VERSION
AZ606329.1 GI:11728519
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```



```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0428 row: K column: 07
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
FEATURES
Location/Qualifiers
1. .32
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0428K07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      16 g      16 t
ORIGIN
Query Match      0.5%; Score 27.2; DB 17; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.5e+05;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACCA 2342
||||||| ||| ||||||||| ||| |||
Db 32 ACACACACACACACACACACACACACACCA 1

RESULT 20
AZ834388/c
LOCUS
DEFINITION
A2834388 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0117N01 F, DNA sequence.
ACCESSION
A2834388
VERSION
A2834388.1 GI:13004296
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0428 row: K column: 07
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
FEATURES
Location/Qualifiers
1. .32
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0428K07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      16 g      16 t
ORIGIN
Query Match      0.5%; Score 27.2; DB 17; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.5e+05;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2311 ACACACACACACACACACACACACACACCA 2342
||||||| ||| ||||||||| ||| |||
Db 32 ACACACACACACACACACACACACACACCA 1

RESULT 20
AZ834388/c
LOCUS
DEFINITION
A2834388 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0117N01 F, DNA sequence.
ACCESSION
A2834388
VERSION
A2834388.1 GI:13004296
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: N column: 01
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
FEATURES
Location/Qualifiers
1. .33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0117N01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      1 a      0 c      17 g      15 t
ORIGIN
Query Match      0.5%; Score 27.2; DB 17; Length 33;
Best Local Similarity 90.6%; Pred. No. 5.5e+05;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAC 2341
||||||| ||| ||||||||| ||| |||
Db 33 CACACACACACACACACACACACACACAC 2

RESULT 21
AZ373001/c
LOCUS
DEFINITION
AZ373001 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0125A12 F, DNA sequence.
ACCESSION
AZ373001
VERSION
AZ373001.1 GI:10486701
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```



## REFERENCE AUTHORS

1 (bases 1 to 36)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0125 row: A column: 12  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 36.

## FEATURES

Location/Qualifiers  
1. .36  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGICM0125A12"  
/clone\_lib="Mouse 10Kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gii4732114[gbiAF129072.1]), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

1 c 18 q 17 t

BASE COUNT  
ORIGIN

0.5%; Score 27.2; DB 17; Length 36;  
ty 90.6%; Pred. No. 5.5e+05;  
ervative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 22  
A7648468/C

	AZ648468	36 bp DNA linear	GSS 14-DEC-2000
ION	IM0517E02R Mouse 10kb plasmid clone UUGC1M0517E02 R,	DNA library Mus musculus genomic	
ON	AZ648468		
S	AZ648468.1 GI:11780965 GSS.		
ISM		house mouse, Mus musculus	

REFERENCE  
AUTHORS

1 (bases 1 to 36)  
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,  
Istait,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10xb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0517 row: E column: 02  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 36

## FEATURES

```

ity sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0517E02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab="Host": E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptorized DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gl14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid pL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorized mouse DNA was annealed to
adaptorized vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
1 c 18 17 +

```

	BASE COUNT	ORIGIN
1	0	0
2	0	0
3	0	0
4	0	0
5	0	0
6	0	0
7	0	0
8	0	0
9	0	0
10	0	0
11	0	0
12	0	0
13	0	0
14	0	0
15	0	0
16	0	0
17	0	0
18	0	0
19	0	0
20	0	0
21	0	0
22	0	0
23	0	0
24	0	0
25	0	0
26	0	0
27	0	0
28	0	0
29	0	0
30	0	0
31	0	0
32	0	0
33	0	0
34	0	0
35	0	0
36	0	0
37	0	0
38	0	0
39	0	0
40	0	0
41	0	0
42	0	0
43	0	0
44	0	0
45	0	0
46	0	0
47	0	0
48	0	0
49	0	0
50	0	0
51	0	0
52	0	0
53	0	0
54	0	0
55	0	0
56	0	0
57	0	0
58	0	0
59	0	0
60	0	0
61	0	0
62	0	0
63	0	0
64	0	0
65	0	0
66	0	0
67	0	0
68	0	0
69	0	0
70	0	0
71	0	0
72	0	0
73	0	0
74	0	0
75	0	0
76	0	0
77	0	0
78	0	0
79	0	0
80	0	0
81	0	0
82	0	0
83	0	0
84	0	0
85	0	0
86	0	0
87	0	0
88	0	0
89	0	0
90	0	0
91	0	0
92	0	0
93	0	0
94	0	0
95	0	0
96	0	0
97	0	0
98	0	0
99	0	0
100	0	0

ty	0.5%;	Score	27.2;	DB	17;	Length	36;
ty	90.6%;	Pred.	No. 5.5e+05;				
ervative	0:	Mismatches	3:	Indels	0:	Gaps	0:

RESULT 23

RESULT 23	AZ848143/c	LOCUS	2M0149A17	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic	linear	GSS 21-FEB-2001
DEFINITION							
ACCESSION	AZ848143						
VERSION	AZ848143.1						
KEYWORDS							
SOURCE	house mouse.						
ORGANISM	Mus musculus						
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.						





REFERENCE  
AUTHORS

1 (bases 1 to 37)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0215 row: L column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 37.

FEATURES  
source

1..37  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0215L08"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

3 a 0 c 17 g 17 t  
Query Match 0.5%; Score 27; DB 17; Length 37;  
Best Local Similarity 85.7%; Pred. No. 6e+05;  
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAT 2344  
||||||| ||| ||||||||| ||| |||  
DB 35 CACACACACACACACACACACACACACTTAT 1

RESULT 28  
AZ305049/c

LOCUS 40 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0005B05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0005B05 R, DNA sequence.

## ACCESSION

AZ305049

## VERSION

AZ305049.1 GI:10341678

## KEYWORDS

GSS.  
house mouse.

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 40)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0005 row: B column: 05  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 40.

FEATURES  
source

1..40  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0005B05"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

1 a 0 c 19 g 20 t  
Query Match 0.5%; Score 27; DB 17; Length 40;  
Best Local Similarity 85.7%; Pred. No. 5.9e+05;  
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACAT 2344  
||||||| ||| ||||||||| ||| |||  
DB 35 CACACACACACACACACACACACACACAT 1

RESULT 29  
AZ475919/c

LOCUS 30 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0294P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0294P15 F, DNA sequence.

## ACCESSION

AZ475919

## VERSION

AZ475919.1 GI:10634044

## KEYWORDS

GSS.  
house mouse.

## SOURCE

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



REFERENCE  
AUTHORS 1 (bases 1 to 30)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0230 row: G column: 12  
Seq primer: CACACAGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 30.  
Location/Qualifiers  
1. .30

FEATURES  
source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0230G12"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 14 g 15 t  
ORIGIN  
Query Match 0.5%; Score 26.8; DB 17; Length 30;  
Best Local Similarity 93.3%; Pred. No. 6.8e+05;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2308 ATCACACACACACACACACACACACACA 2337  
|||||  
Db 30 ATCACACACACACACACACACACACACA 1

RESULT 32  
AZ459099/c  
LOCUS AZ459099 31 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0263012R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0263012 R, DNA sequence.  
ACCESSION AZ459099  
VERSION AZ459099.1 GI:10617224  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS 1 (bases 1 to 31)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0263 row: O column: 12  
Seq primer: CACACAGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31

FEATURES  
source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0263012"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 16 g 15 t  
ORIGIN  
Query Match 0.5%; Score 26.8; DB 17; Length 31;  
Best Local Similarity 93.3%; Pred. No. 6.7e+05;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 CACACACACACACACACACACACACACA 2339  
|||||  
Db 31 CACACACACACACACACACACACACACA 2

RESULT 33.  
AZ470636/c  
LOCUS AZ470636 31 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0284N13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0284N13 R, DNA sequence.  
ACCESSION AZ470636  
VERSION AZ470636.1 GI:10628761  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE	1 (bases 1 to 31)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0284 row: N column: 13 Seq primer: CACACAGGAACAACGCTATGACC Class: Plasmid ends High quality sequence stop: 31. Location/Qualifiers 1..31 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGCLM0284N13" /clone_lib="Mouse 10kb plasmid UUGCLM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES	Source
BASE COUNT	0 a 0 c 15 g 16 t
ORIGIN	
Query Match	0.5%; Score 26.8; DB 17; Length 31;
Best Local Similarity	93.3%; Pred. No. 6.7e+05;
Matches	28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2310 CACACACACAGACAGACACACACACACA 2339 
Db	30 CACACACACACACACACACACACACACACA 1
RESULT 34	
AZ479719/c	
LOCUS	AZ479719 31 bp DNA linear GSS 04-OCT-2000
DEFINITION	IM0300N01R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0300N01 R, DNA sequence.
ACCESSION	AZ479719
VERSION	AZ479719.1 GI:10639888
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.









**REFERENCE**  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A., and Wright,D., Weiss,R.  
**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL**  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0269 row: D column: 16  
Seq primer: CACACAGAACACTGATGACC  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0269D16"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT**  
ORIGIN  
16 a 15 c 0 g 0 t  
Query Match 0.5%; Score 26.8; DB 17; Length 31;  
Best Local Similarity 93.3%; Pred. No. 6.7e+05;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Yy** 2310 CACACACACACACACACACACACACACA 2339  
||||||| ||| ||||| ||||| |||||  
2 CACACACACACACACACACACACACACA 31

**Db**

**RESULT 40**  
AZ307970/c  
**LOCUS**  
A2307970 32 bp DNA linear GSS 29-SEP-2000  
DEFINITION  
1M0010A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0010A03 R, DNA sequence.  
ACCESSION  
A2307970  
VERSION  
GI:10347495  
KEYWORDS  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A., and Wright,D., Weiss,R.  
**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL**  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0269 row: D column: 16  
Seq primer: CACACAGAACACTGATGACC  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC2M0269D16"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT**  
ORIGIN  
16 a 15 c 0 g 0 t  
Query Match 0.5%; Score 26.8; DB 17; Length 31;  
Best Local Similarity 93.3%; Pred. No. 6.7e+05;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Yy** 2310 CACACACACACACACACACACACACACA 2339  
||||||| ||| ||||| ||||| |||||  
2 CACACACACACACACACACACACACACA 31

**Db**

**RESULT 41**  
AZ311840/c  
**LOCUS**  
A2311840 32 bp DNA linear GSS 29-SEP-2000  
DEFINITION  
1M0027M21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0027M21 F, DNA sequence.  
ACCESSION  
A2311840  
VERSION  
GI:10355201  
KEYWORDS  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.







REFERENCE  
AUTHORS

1 (bases 1 to 33)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0461 row: G column: 04

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 33.

FEATURES  
source

Location/Qualifiers

1..33

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0461G04"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."BASE COUNT  
ORIGIN

0 a 0 c 17 g 16 t

Query Match

0.5%; Score 26.8; DB 17; Length 33;

Best Local Similarity 93.3%; Pred. No. 6.7e+05;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2310 CACACACACACACACACACACACACACA 2339

|||||

Db 33 CACACACACACACACACACACACACACA 4

## RESULT 48

AZ623817/c

LOCUS

1M0461G24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0461G24 R, DNA sequence.

ACCESSION

AZ623817.1 GI:11746007

KEYWORDS

GSS.

SOURCE

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 33)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT

Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0461 row: G column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 33.

FEATURES  
Source

Location/Qualifiers

1..33

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0461G24"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."BASE COUNT  
ORIGIN

0 a 0 c 17 g 16 t

Query Match

0.5%; Score 26.8; DB 17; Length 33;

Best Local Similarity 93.3%; Pred. No. 6.7e+05;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2310 CACACACACACACACACACACACACACA 2339

|||||

Db 33 CACACACACACACACACACACACACACA 4

## RESULT 49

AZ817793/c

LOCUS

2M0087P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0087P19 F, DNA sequence.

ACCESSION

AZ817793.1 GI:12987701

KEYWORDS

GSS.

SOURCE

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



